

#8

SEQUENCE LISTING

RECEIVED
MAY 03 2002
TECH CENTER 1600/2900

<110> Giuliano, Kenneth A.
Bright, Gary
Olson, Keith
Burroughs-Tencza, Sarah

<120> A System for Cell Based Screening

<130> 97-022-K2

<140> 09/713,572

<141> 2000-11-15

<150> 09/430,656

<151> 1999-10-29

<150> 09/398,965

<151> 1999-09-17

<150> 09/031,271

<151> 1998-02-27

<150> 08/810,983

<151> 1997-02-27

<150> 60/136,078

<151> 1999-05-26

<150> 60/106,308

<151> 1998-10-30

<160> 168

<170> PatentIn Ver. 2.0

<210> 1

<211> 1770

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) .. (882)

<220>

<223> Description of Artificial Sequence:

GFP-DEVD-Annexin II construct

<400> 1

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag tcc 720
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240

gga ctc aga tct ggc gcc ggc gct gga gcc gga gct ggc gcc gga gcc 768
 Gly Leu Arg Ser Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala
 245 250 255

gac gag gtg gac ggc gcc ggc gcc gat gaa gta gat ggc gcc atg tct 816
 Asp Glu Val Asp Gly Ala Gly Ala Asp Glu Val Asp Gly Ala Met Ser
 260 265 270

act gtc cac gaa atc ctg tgc aag ctc agc ttg gag ggt gat cat tct 864
 Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp His Ser
 275 280 285

aca ccc cca agt gcc tat tgaatggtga gcaagggcga ggagctgttc 912
 Thr Pro Pro Ser Ala Tyr
 290

accgggggtgg tgcccatcct ggtcgagctg gacggcgacg taaacggcca caagttcagc 972
 gtgtccggcg agggcgaggg cgatgccacc tacggcaagc tgaccctgaa gttcatctgc 1032
 accaccggca agctgcccgt gccctggccc accctcgtga ccaccctgac ctacggcgtg 1092
 cagtgttca gccgctaccc cgaccacatg aagcagcacg acttcttcaa gtccgccatg 1152
 cccgaaggct acgtccagga gcgcaccatc ttcttcaagg acgacggcaa ctacaagacc 1212
 cgcgccgagg tgaagttcga gggcgacacc ctggtgaacc gcatcgagct gaagggcatc 1272
 gacttcaagg aggacggcaa catcctgggg cacaagctgg agtacaacta caacagccac 1332
 aacgtctata tcatggccga caagcagaag aacggcatca aggtgaactt caagatccgc 1392
 cacaacatcg aggacggcag cgtgcagctc gccgaccact accagcagaa ccccccatc 1452
 ggcgacggcc ccgtgctgct gcccgacaac cactacctga gcacccagtc cgccctgagc 1512
 aaagacccca acgagaagcg cgatcacatg gtctctgctgg agttcgtgac cgccgccggg 1572
 atcactctcg gcatggacga gctgtacaag tccggactca gatctggcgc cggcgctgga 1632
 gccggagctg gcgcccggagc cgacgaggtg gacggcgccg gcgcccgatga agtagatggc 1692
 gccatgtcta ctgtccacga aatcctgtgc aagctcagct tggaggggtga tcattctaca 1752
 cccccaagtg cctattga 1770

<210> 2
 <211> 294
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 GFP-DEVD-Annexin II construct

<400> 2
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Ser
 225 230 235 240
 Gly Leu Arg Ser Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala
 245 250 255
 Asp Glu Val Asp Gly Ala Gly Ala Asp Glu Val Asp Gly Ala Met Ser
 260 265 270
 Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Asp His Ser
 275 280 285
 Thr Pro Pro Ser Ala Tyr
 290

<210> 3
 <211> 2439
 <212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(2436)

<220>

<223> Description of Artificial Sequence:

EYFP-DEV D-MAPKDM construct

<400> 3

atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly

| 180 | | | | | | | | | | 185 | | | | | | | | | | 190 | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|--|--|-----|--|--|--|--|--|--|--|--|--|--|
| ccc | gtg | ctg | ctg | ccc | gac | aac | cac | tac | ctg | agc | tac | cag | tcc | gcc | ctg | 624 | | | | | | | | | | | | | | |
| Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | Tyr | Gln | Ser | Ala | Leu | | | | | | | | | | | | | | | |
| 195 | | | | | 200 | | | | | 205 | | | | | | | | | | | | | | | | | | | | |
| agc | aaa | gac | ccc | aac | gag | aag | cgc | gat | cac | atg | gtc | ctg | ctg | gag | ttc | 672 | | | | | | | | | | | | | | |
| Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu | Leu | Glu | Phe | | | | | | | | | | | | | | | |
| 210 | | | | | 215 | | | | | 220 | | | | | | | | | | | | | | | | | | | | |
| gtg | acc | gcc | gcc | ggg | atc | act | ctc | ggc | atg | gac | gag | ctg | tac | aag | aag | 720 | | | | | | | | | | | | | | |
| Val | Thr | Ala | Ala | Gly | Ile | Thr | Leu | Gly | Met | Asp | Glu | Leu | Tyr | Lys | Lys | | | | | | | | | | | | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | | | | | | | | | | | | | | |
| gga | gac | gaa | gtg | gac | gga | gcc | gac | ctc | agt | ctt | gtg | gat | gcg | ttg | aca | 768 | | | | | | | | | | | | | | |
| Gly | Asp | Glu | Val | Asp | Gly | Ala | Asp | Leu | Ser | Leu | Val | Asp | Ala | Leu | Thr | | | | | | | | | | | | | | | |
| 245 | | | | | 250 | | | | | 255 | | | | | | | | | | | | | | | | | | | | |
| gaa | cca | cct | cca | gaa | att | gag | gga | gaa | ata | aag | cga | gac | ttc | atg | gct | 816 | | | | | | | | | | | | | | |
| Glu | Pro | Pro | Pro | Glu | Ile | Glu | Gly | Glu | Ile | Lys | Arg | Asp | Phe | Met | Ala | | | | | | | | | | | | | | | |
| 260 | | | | | 265 | | | | | 270 | | | | | | | | | | | | | | | | | | | | |
| gcg | ctg | gag | gca | gag | ccc | tat | gat | gac | atc | gtg | gga | gaa | act | gtg | gag | 864 | | | | | | | | | | | | | | |
| Ala | Leu | Glu | Ala | Glu | Pro | Tyr | Asp | Asp | Ile | Val | Gly | Glu | Thr | Val | Glu | | | | | | | | | | | | | | | |
| 275 | | | | | 280 | | | | | 285 | | | | | | | | | | | | | | | | | | | | |
| aaa | act | gag | ttt | att | cct | ctc | ctg | gat | ggg | gat | gag | aaa | acc | ggg | aac | 912 | | | | | | | | | | | | | | |
| Lys | Thr | Glu | Phe | Ile | Pro | Leu | Leu | Asp | Gly | Asp | Glu | Lys | Thr | Gly | Asn | | | | | | | | | | | | | | | |
| 290 | | | | | 295 | | | | | 300 | | | | | | | | | | | | | | | | | | | | |
| tca | gag | tcc | aaa | aag | aaa | ccc | tgc | tta | gac | act | agc | cag | gtt | gaa | ggg | 960 | | | | | | | | | | | | | | |
| Ser | Glu | Ser | Lys | Lys | Lys | Pro | Cys | Leu | Asp | Thr | Ser | Gln | Val | Glu | Gly | | | | | | | | | | | | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | | | | | | | | | | | | | | |
| atc | cca | tct | tct | aaa | cca | aca | ctc | cta | gcc | aat | ggg | gat | cat | gga | atg | 1008 | | | | | | | | | | | | | | |
| Ile | Pro | Ser | Ser | Lys | Pro | Thr | Leu | Leu | Ala | Asn | Gly | Asp | His | Gly | Met | | | | | | | | | | | | | | | |
| 325 | | | | | 330 | | | | | 335 | | | | | | | | | | | | | | | | | | | | |
| gag | ggg | aat | aac | act | gca | ggg | tct | cca | act | gac | ttc | ctt | gaa | gag | aga | 1056 | | | | | | | | | | | | | | |
| Glu | Gly | Asn | Asn | Thr | Ala | Gly | Ser | Pro | Thr | Asp | Phe | Leu | Glu | Glu | Arg | | | | | | | | | | | | | | | |
| 340 | | | | | 345 | | | | | 350 | | | | | | | | | | | | | | | | | | | | |
| gtg | gac | tat | ccg | gat | tat | cag | agc | agc | cag | aac | tgg | cca | gaa | gat | gca | 1104 | | | | | | | | | | | | | | |
| Val | Asp | Tyr | Pro | Asp | Tyr | Gln | Ser | Ser | Gln | Asn | Trp | Pro | Glu | Asp | Ala | | | | | | | | | | | | | | | |
| 355 | | | | | 360 | | | | | 365 | | | | | | | | | | | | | | | | | | | | |
| agc | ttt | tgt | ttc | cag | cct | cag | caa | gtg | tta | gat | act | gac | cag | gct | gag | 1152 | | | | | | | | | | | | | | |
| Ser | Phe | Cys | Phe | Gln | Pro | Gln | Gln | Val | Leu | Asp | Thr | Asp | Gln | Ala | Glu | | | | | | | | | | | | | | | |
| 370 | | | | | 375 | | | | | 380 | | | | | | | | | | | | | | | | | | | | |
| ccc | ttt | aac | gag | cac | cgt | gat | gat | ggg | ttg | gca | gat | ctg | ctc | ttt | gtc | 1200 | | | | | | | | | | | | | | |
| Pro | Phe | Asn | Glu | His | Arg | Asp | Asp | Gly | Leu | Ala | Asp | Leu | Leu | Phe | Val | | | | | | | | | | | | | | | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | | | | | | | | | | | | | | | |
| tcc | agt | gga | ccc | acg | aac | gct | tct | gca | ttt | aca | gag | cga | gac | aat | cct | 1248 | | | | | | | | | | | | | | |
| Ser | Ser | Gly | Pro | Thr | Asn | Ala | Ser | Ala | Phe | Thr | Glu | Arg | Asp | Asn | Pro | | | | | | | | | | | | | | | |
| 405 | | | | | 410 | | | | | 415 | | | | | | | | | | | | | | | | | | | | |

B1

| | |
|---|------|
| tca gaa gac agt tac ggt atg ctt ccc tgt gac tca ttt gct tcc acg | 1296 |
| Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser Thr | |
| 420 425 430 | |
| gct gtt gta tct cag gag tgg tct gtg gga gcc cca aac tct cca tgt | 1344 |
| Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys | |
| 435 440 445 | |
| tca gag tcc tgt gtc tcc cca gag gtt act ata gaa acc cta cag cca | 1392 |
| Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro | |
| 450 455 460 | |
| gca aca gag ctc tcc aag gca gca gaa gtg gaa tca gtg aaa gag cag | 1440 |
| Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln | |
| 465 470 475 480 | |
| ctg cca gct aaa gca ttg gaa acg atg gca gag cag acc act gat gtg | 1488 |
| Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val | |
| 485 490 495 | |
| gtg cac tct cca tcc aca gac aca aca cca ggc cca gac aca gag gca | 1536 |
| Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala | |
| 500 505 510 | |
| gca ctg gct aaa gac ata gaa gag atc acc aag cca gat gtg ata ttg | 1584 |
| Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu | |
| 515 520 525 | |
| gca aat gtc acg cag cca tct act gaa tcg gat atg ttc ctg gcc cag | 1632 |
| Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln | |
| 530 535 540 | |
| gac atg gaa cta ctc aca gga aca gag gca gcc cac gct aac aat atc | 1680 |
| Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile | |
| 545 550 555 560 | |
| ata ttg cct aca gaa cca gac gaa tct tca acc aag gat gta gca cca | 1728 |
| Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro | |
| 565 570 575 | |
| cct atg gaa gaa gaa att gtc cca ggc aat gat acg aca tcc ccc aaa | 1776 |
| Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys | |
| 580 585 590 | |
| gaa aca gag aca aca ctt cca ata aaa atg gac ttg gca cca cct gag | 1824 |
| Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu | |
| 595 600 605 | |
| gat gtg tta ctt acc aaa gaa aca gaa cta gcc cca gcc aag ggc atg | 1872 |
| Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met | |
| 610 615 620 | |
| gtt tca ctc tca gaa ata gaa gag gct ctg gca aag aat gat gtt cgc | 1920 |
| Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg | |
| 625 630 635 640 | |

| | |
|---|------|
| tct gca gaa ata cct gtg gct cag gag aca gtg gtc tca gaa aca gag | 1968 |
| Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu | |
| 645 650 655 | |
| gtg gtc ctg gca aca gaa gtg gta ctg ccc tca gat ccc ata aca aca | 2016 |
| Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr | |
| 660 665 670 | |
| ttg aca aag gat gtg aca ctc ccc tta gaa gca gag aga ccg ttg gtg | 2064 |
| Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val | |
| 675 680 685 | |
| acg gac atg act cca tct ctg gaa aca gaa atg acc cta ggc aaa gag | 2112 |
| Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu | |
| 690 695 700 | |
| aca gct cca ccc aca gaa aca aat ttg ggc atg gcc aaa gac atg tct | 2160 |
| Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser | |
| 705 710 715 720 | |
| cca ctc cca gaa tca gaa gtg act ctg ggc aag gac gtg gtt ata ctt | 2208 |
| Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu | |
| 725 730 735 | |
| cca gaa aca aag gtg gct gag ttt aac aat gtg act cca ctt tca gaa | 2256 |
| Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu | |
| 740 745 750 | |
| gaa gag gta acc tca gtc aag gac atg tct ccg tct gca gaa aca gag | 2304 |
| Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu | |
| 755 760 765 | |
| gct ccc ctg gct aag aat gct gat ctg cac tca gga aca gag ctg att | 2352 |
| Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile | |
| 770 775 780 | |
| gtg gac aac agc atg gct cca gcc tcc gat ctt gca ctg ccc ttg gaa | 2400 |
| Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu | |
| 785 790 795 800 | |
| aca aaa gta gca aca gtt cca att aaa gac aaa gga tga | 2439 |
| Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly | |
| 805 810 | |

<210> 4
 <211> 812
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 EYFP-DEVD-MAPKDM construct

<400> 4
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Lys
 225 230 235 240
 Gly Asp Glu Val Asp Gly Ala Asp Leu Ser Leu Val Asp Ala Leu Thr
 245 250 255
 Glu Pro Pro Pro Glu Ile Glu Gly Glu Ile Lys Arg Asp Phe Met Ala
 260 265 270
 Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val Gly Glu Thr Val Glu
 275 280 285
 Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn
 290 295 300
 Ser Glu Ser Lys Lys Lys Pro Cys Leu Asp Thr Ser Gln Val Glu Gly
 305 310 315 320

Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn Gly Asp His Gly Met
 325 330 335
 Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg
 340 345 350
 Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala
 355 360 365
 Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp Thr Asp Gln Ala Glu
 370 375 380
 Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe Val
 385 390 395 400
 Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro
 405 410 415
 Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser Thr
 420 425 430
 Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys
 435 440 445
 Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro
 450 455 460
 Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln
 465 470 475 480
 Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val
 485 490 495
 Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala
 500 505 510
 Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu
 515 520 525
 Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln
 530 535 540
 Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile
 545 550 555 560
 Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro
 565 570 575
 Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys
 580 585 590
 Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu
 595 600 605
 Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met
 610 615 620

Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg
 625 630 635 640
 Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu
 645 650 655
 Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr
 660 665 670
 Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val
 675 680 685
 Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu
 690 695 700
 Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser
 705 710 715 720
 Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu
 725 730 735
 Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu
 740 745 750
 Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu
 755 760 765
 Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile
 770 775 780
 Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu
 785 790 795 800
 Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly
 805 810

<210> 5
 <211> 2439
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(2436)

<220>
 <223> Description of Artificial Sequence:
 EYFP-DEAD-MAPKDM construct

<400> 5
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Glu | Leu | Asp | Gly | Asp | Val | Asn | Gly | His | Lys | Phe | Ser | Val | Ser | Gly | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| gag | ggc | gag | ggc | gat | gcc | acc | tac | ggc | aag | ctg | acc | ctg | aag | ttc | atc | 144 | |
| Glu | Gly | Glu | Gly | Asp | Ala | Thr | Tyr | Gly | Lys | Leu | Thr | Leu | Lys | Phe | Ile | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| tgc | acc | acc | ggc | aag | ctg | ccc | gtg | ccc | tgg | ccc | acc | ctc | gtg | acc | acc | 192 | |
| Cys | Thr | Thr | Gly | Lys | Leu | Pro | Val | Pro | Trp | Pro | Thr | Leu | Val | Thr | Thr | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| ttc | ggc | tac | ggc | ctg | cag | tgc | ttc | gcc | cgc | tac | ccc | gac | cac | atg | aag | 240 | |
| Phe | Gly | Tyr | Gly | Leu | Gln | Cys | Phe | Ala | Arg | Tyr | Pro | Asp | His | Met | Lys | | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | | |
| cag | cac | gac | ttc | ttc | aag | tcc | gcc | atg | ccc | gaa | ggc | tac | gtc | cag | gag | 288 | |
| Gln | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro | Glu | Gly | Tyr | Val | Gln | Glu | | |
| | | | 85 | | | | | | 90 | | | | | 95 | | | |
| cgc | acc | atc | ttc | ttc | aag | gac | gac | ggc | aac | tac | aag | acc | cgc | gcc | gag | 336 | |
| Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn | Tyr | Lys | Thr | Arg | Ala | Glu | | |
| | | 100 | | | | | | 105 | | | | | 110 | | | | |
| gtg | aag | ttc | gag | ggc | gac | acc | ctg | gtg | aac | cgc | atc | gag | ctg | aag | ggc | 384 | |
| Val | Lys | Phe | Glu | Gly | Asp | Thr | Leu | Val | Asn | Arg | Ile | Glu | Leu | Lys | Gly | | |
| | 115 | | | | | 120 | | | | | | 125 | | | | | |
| atc | gac | ttc | aag | gag | gac | ggc | aac | atc | ctg | ggg | cac | aag | ctg | gag | tac | 432 | |
| Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu | Gly | His | Lys | Leu | Glu | Tyr | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |
| aac | tac | aac | agc | cac | aac | gtc | tat | atc | atg | gcc | gac | aag | cag | aag | aac | 480 | |
| Asn | Tyr | Asn | Ser | His | Asn | Val | Tyr | Ile | Met | Ala | Asp | Lys | Gln | Lys | Asn | | |
| 145 | | | | | 150 | | | | 155 | | | | | | 160 | | |
| ggc | atc | aag | gtg | aac | ttc | aag | atc | cgc | cac | aac | atc | gag | gac | ggc | agc | 528 | |
| Gly | Ile | Lys | Val | Asn | Phe | Lys | Ile | Arg | His | Asn | Ile | Glu | Asp | Gly | Ser | | |
| | | | 165 | | | | | 170 | | | | | | 175 | | | |
| gtg | cag | ctc | gcc | gac | cac | tac | cag | cag | aac | acc | ccc | atc | ggc | gac | ggc | 576 | |
| Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn | Thr | Pro | Ile | Gly | Asp | Gly | | |
| | | 180 | | | | | 185 | | | | | | 190 | | | | |
| ccc | gtg | ctg | ctg | ccc | gac | aac | cac | tac | ctg | agc | tac | cag | tcc | gcc | ctg | 624 | |
| Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | Tyr | Gln | Ser | Ala | Leu | | |
| | | 195 | | | | 200 | | | | | | 205 | | | | | |
| agc | aaa | gac | ccc | aac | gag | aag | cgc | gat | cac | atg | gtc | ctg | ctg | gag | ttc | 672 | |
| Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu | Leu | Glu | Phe | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| gtg | acc | gcc | gcc | ggg | atc | act | ctc | ggc | atg | gac | gag | ctg | tac | aag | ccc | 720 | |
| Val | Thr | Ala | Ala | Gly | Ile | Thr | Leu | Gly | Met | Asp | Glu | Leu | Tyr | Lys | Pro | | |
| 225 | | | | | 230 | | | | 235 | | | | | | 240 | | |
| aga | gac | gaa | gcc | gac | agc | gcc | gac | ctc | agt | ctt | gtg | gat | gcg | ttg | aca | 768 | |
| Arg | Asp | Glu | Ala | Asp | Ser | Ala | Asp | Leu | Ser | Leu | Val | Asp | Ala | Leu | Thr | | |

| 245 | | | | | | | | | | 250 | | | | | | | | | | 255 | | | | | | | | | | |
|---|------|--|--|--|--|--|--|--|--|-----|--|--|--|--|--|--|--|--|--|-----|--|--|--|--|--|--|--|--|--|--|
| gaa cca cct cca gaa att gag gga gaa ata aag cga gac ttc atg gct | 816 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Glu Pro Pro Pro Glu Ile Glu Gly Glu Ile Lys Arg Asp Phe Met Ala | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 260 265 270 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gcg ctg gag gca gag ccc tat gat gac atc gtg gga gaa act gtg gag | 864 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val Gly Glu Thr Val Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 275 280 285 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| aaa act gag ttt att cct ctc ctg gat ggt gat gag aaa acc ggg aac | 912 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 290 295 300 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tca gag tcc aaa aag aaa ccc tgc tta gac act agc cag gtt gaa ggt | 960 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ser Glu Ser Lys Lys Lys Pro Cys Leu Asp Thr Ser Gln Val Glu Gly | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 305 310 315 320 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| atc cca tct tct aaa cca aca ctc cta gcc aat ggt gat cat gga atg | 1008 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn Gly Asp His Gly Met | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 325 330 335 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gag ggg aat aac act gca ggg tct cca act gac ttc ctt gaa gag aga | 1056 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 340 345 350 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gtg gac tat ccg gat tat cag agc agc cag aac tgg cca gaa gat gca | 1104 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 355 360 365 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| agc ttt tgt ttc cag cct cag caa gtg tta gat act gac cag gct gag | 1152 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp Thr Asp Gln Ala Glu | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 370 375 380 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| ccc ttt aac gag cac cgt gat gat ggt ttg gca gat ctg ctc ttt gtc | 1200 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe Val | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 385 390 395 400 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tcc agt gga ccc acg aac gct tct gca ttt aca gag cga gac aat cct | 1248 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 405 410 415 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tca gaa gac agt tac ggt atg ctt ccc tgt gac tca ttt gct tcc acg | 1296 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser Thr | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 420 425 430 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gct gtt gta tct cag gag tgg tct gtg gga gcc cca aac tct cca tgt | 1344 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 435 440 445 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| tca gag tcc tgt gtc tcc cca gag gtt act ata gaa acc cta cag cca | 1392 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 450 455 460 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| gca aca gag ctc tcc aag gca gca gaa gtg gaa tca gtg aaa gag cag | 1440 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 465 470 475 480 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

ctg cca gct aaa gca ttg gaa acg atg gca gag cag acc act gat gtg 1488
 Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val
 485 490 495

gtg cac tct cca tcc aca gac aca aca cca ggc cca gac aca gag gca 1536
 Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala
 500 505 510

gca ctg gct aaa gac ata gaa gag atc acc aag cca gat gtg ata ttg 1584
 Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu
 515 520 525

gca aat gtc acg cag cca tct act gaa tcg gat atg ttc ctg gcc cag 1632
 Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln
 530 535 540

gac atg gaa cta ctc aca gga aca gag gca gcc cac gct aac aat atc 1680
 Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile
 545 550 555 560

ata ttg cct aca gaa cca gac gaa tct tca acc aag gat gta gca cca 1728
 Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro
 565 570 575

cct atg gaa gaa gaa att gtc cca ggc aat gat acg aca tcc ccc aaa 1776
 Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys
 580 585 590

gaa aca gag aca aca ctt cca ata aaa atg gac ttg gca cca cct gag 1824
 Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu
 595 600 605

gat gtg tta ctt acc aaa gaa aca gaa cta gcc cca gcc aag ggc atg 1872
 Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met
 610 615 620

gtt tca ctc tca gaa ata gaa gag gct ctg gca aag aat gat gtt cgc 1920
 Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg
 625 630 635 640

tct gca gaa ata cct gtg gct cag gag aca gtg gtc tca gaa aca gag 1968
 Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu
 645 650 655

gtg gtc ctg gca aca gaa gtg gta ctg ccc tca gat ccc ata aca aca 2016
 Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr
 660 665 670

ttg aca aag gat gtg aca ctc ccc tta gaa gca gag aga ccg ttg gtg 2064
 Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val
 675 680 685

acg gac atg act cca tct ctg gaa aca gaa atg acc cta ggc aaa gag 2112
 Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu
 690 695 700

aca gct cca ccc aca gaa aca aat ttg ggc atg gcc aaa gac atg tct 2160
 Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser
 705 710 715 720
 cca ctc cca gaa tca gaa gtg act ctg ggc aag gac gtg gtt ata ctt 2208
 Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu
 725 730 735
 cca gaa aca aag gtg gct gag ttt aac aat gtg act cca ctt tca gaa 2256
 Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu
 740 745 750
 gaa gag gta acc tca gtc aag gac atg tct ccg tct gca gaa aca gag 2304
 Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu
 755 760 765
 gct ccc ctg gct aag aat gct gat ctg cac tca gga aca gag ctg att 2352
 Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile
 770 775 780
 gtg gac aac agc atg gct cca gcc tcc gat ctt gca ctg ccc ttg gaa 2400
 Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu
 785 790 795 800
 aca aaa gta gca aca gtt cca att aaa gac aaa gga tga 2439
 Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly
 805 810

<210> 6

<211> 812

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

EYFP-DEAD-MAPKDM construct

<400> 6

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Pro
 225 230 235 240
 Arg Asp Glu Ala Asp Ser Ala Asp Leu Ser Leu Val Asp Ala Leu Thr
 245 250 255
 Glu Pro Pro Pro Glu Ile Glu Gly Glu Ile Lys Arg Asp Phe Met Ala
 260 265 270
 Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val Gly Glu Thr Val Glu
 275 280 285
 Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn
 290 295 300
 Ser Glu Ser Lys Lys Lys Pro Cys Leu Asp Thr Ser Gln Val Glu Gly
 305 310 315 320
 Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn Gly Asp His Gly Met
 325 330 335
 Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg
 340 345 350
 Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala
 355 360 365
 Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp Thr Asp Gln Ala Glu
 370 375 380
 Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe Val
 385 390 395 400

Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro
 405 410 415
 Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser Thr
 420 425 430
 Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys
 435 440 445
 Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro
 450 455 460
 Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln
 465 470 475 480
 Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val
 485 490 495
 Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala
 500 505 510
 Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu
 515 520 525
 Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln
 530 535 540
 Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile
 545 550 555 560
 Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro
 565 570 575
 Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys
 580 585 590
 Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu
 595 600 605
 Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met
 610 615 620
 Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg
 625 630 635 640
 Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu
 645 650 655
 Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr
 660 665 670
 Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val
 675 680 685
 Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu
 690 695 700

Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser
 705 710 715 720
 Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu
 725 730 735
 Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu
 740 745 750
 Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu
 755 760 765
 Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile
 770 775 780
 Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu
 785 790 795 800
 Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly
 805 810

<210> 7
 <211> 864
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1) .. (861)

<220>
 <223> Description of Artificial Sequence: F25-MEK1
 construct

<400> 7
 atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro | Glu | Gly | Tyr | Val | Gln | Glu | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| agg | acc | atc | ttc | ttc | aaa | gat | gac | ggc | aac | tac | aag | aca | cgt | gct | gaa | 336 |
| Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn | Tyr | Lys | Thr | Arg | Ala | Glu | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| gtc | aag | ttt | gaa | ggt | gat | acc | ctt | gtt | aat | aga | atc | gag | tta | aaa | ggt | 384 |
| Val | Lys | Phe | Glu | Gly | Asp | Thr | Leu | Val | Asn | Arg | Ile | Glu | Leu | Lys | Gly | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| att | gac | ttc | aag | gaa | gat | ggc | aac | att | ctg | gga | cac | aaa | ttg | gaa | tac | 432 |
| Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu | Gly | His | Lys | Leu | Glu | Tyr | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| aac | tat | aac | tca | cac | aat | gta | tac | atc | atg | gca | gac | aaa | caa | aag | aat | 480 |
| Asn | Tyr | Asn | Ser | His | Asn | Val | Tyr | Ile | Met | Ala | Asp | Lys | Gln | Lys | Asn | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| gga | atc | aaa | gtg | aac | ttc | aag | acc | cgc | cac | aac | att | gaa | gat | gga | agc | 528 |
| Gly | Ile | Lys | Val | Asn | Phe | Lys | Thr | Arg | His | Asn | Ile | Glu | Asp | Gly | Ser | |
| | | | 165 | | | | | 170 | | | | | | 175 | | |
| gtt | caa | cta | gca | gac | cat | tat | caa | caa | aat | act | cca | att | ggc | gat | ggc | 576 |
| Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn | Thr | Pro | Ile | Gly | Asp | Gly | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| cct | gtc | ctt | tta | cca | gac | aac | cat | tac | ctg | tcc | aca | caa | tct | gcc | ctt | 624 |
| Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | Thr | Gln | Ser | Ala | Leu | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| tcg | aaa | gat | ccc | aac | gaa | aag | aga | gac | cac | atg | gtc | ctt | ctt | gag | ttt | 672 |
| Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu | Leu | Glu | Phe | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| gta | aca | gct | gct | ggg | att | aca | cat | ggc | atg | gat | gaa | ctg | tac | aac | acc | 720 |
| Val | Thr | Ala | Ala | Gly | Ile | Thr | His | Gly | Met | Asp | Glu | Leu | Tyr | Asn | Thr | |
| 225 | | | | 230 | | | | 235 | | | | | | | 240 | |
| ggt | atg | ccc | aag | aag | aag | ccg | acg | ccc | atc | cag | ctg | aac | ccg | gcc | ccc | 768 |
| Gly | Met | Pro | Lys | Lys | Lys | Pro | Thr | Pro | Ile | Gln | Leu | Asn | Pro | Ala | Pro | |
| | | | 245 | | | | | 250 | | | | | 255 | | | |
| gac | ggc | tct | gca | gtt | aac | ggg | acc | agc | tct | gcg | gag | acc | aac | ttg | gag | 816 |
| Asp | Gly | Ser | Ala | Val | Asn | Gly | Thr | Ser | Ser | Ala | Glu | Thr | Asn | Leu | Glu | |
| | | | 260 | | | | 265 | | | | | | 270 | | | |
| gcc | ttg | cag | aag | aag | ctg | gag | gag | cta | gag | ctt | gat | gag | cag | cag | tga | 864 |
| Ala | Leu | Gln | Lys | Lys | Leu | Glu | Glu | Leu | Glu | Leu | Asp | Glu | Gln | Gln | | |
| | | 275 | | | | 280 | | | | | | 285 | | | | |

<210> 8

<211> 287

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: F25-MEK1
construct

<400> 8

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160
Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
165 170 175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220
Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Thr
225 230 235 240
Gly Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn Pro Ala Pro
245 250 255
Asp Gly Ser Ala Val Asn Gly Thr Ser Ser Ala Glu Thr Asn Leu Glu
260 265 270
Ala Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu Gln Gln

275

280

285

<210> 9

<211> 876

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) .. (873)

<220>

<223> Description of Artificial Sequence: F25-MEK2
construct

<400> 9

| | |
|---|-----|
| atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt | 48 |
| Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu | |
| 1 5 10 15 | |
| ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga | 96 |
| Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly | |
| 20 25 30 | |
| gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc | 144 |
| Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile | |
| 35 40 45 | |
| tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act | 192 |
| Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr | |
| 50 55 60 | |
| ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa | 240 |
| Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys | |
| 65 70 75 80 | |
| cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa | 288 |
| Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu | |
| 85 90 95 | |
| agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa | 336 |
| Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu | |
| 100 105 110 | |
| gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt | 384 |
| Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly | |
| 115 120 125 | |
| att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac | 432 |
| Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr | |
| 130 135 140 | |
| aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat | 480 |
| Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn | |
| 145 150 155 160 | |

| | |
|---|-----|
| gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc | 528 |
| Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser | |
| 165 170 175 | |
| gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc | 576 |
| Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly | |
| 180 185 190 | |
| cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt | 624 |
| Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu | |
| 195 200 205 | |
| tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt | 672 |
| Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe | |
| 210 215 220 | |
| gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac acc | 720 |
| Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Thr | |
| 225 230 235 240 | |
| ggg atg ctg gcc cgg agg aag ccg gtg ctg ccg gcg ctc acc atc aac | 768 |
| Gly Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn | |
| 245 250 255 | |
| cct acc atc gcc gag ggc cca tcc cct acc agc gag ggc gcc tcc gag | 816 |
| Pro Thr Ile Ala Glu Gly Pro Ser Pro Thr Ser Glu Gly Ala Ser Glu | |
| 260 265 270 | |
| gca aac ctg gtg gac ctg cag aag aag ctg gag gag ctg gaa ctt gac | 864 |
| Ala Asn Leu Val Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp | |
| 275 280 285 | |
| gag cag cag taa | 876 |
| Glu Gln Gln | |
| 290 | |

<210> 10
 <211> 291
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: F25-MEK2
 construct

<400> 10
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

| 50 | | | | | 55 | | | | | 60 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Cys | Tyr | Gly | Val | Gln | Cys | Phe | Ser | Arg | Tyr | Pro | Asp | His | Met | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Arg | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro | Glu | Gly | Tyr | Val | Gln | Glu |
| | | | 85 | | | | | | 90 | | | | | 95 | |
| Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn | Tyr | Lys | Thr | Arg | Ala | Glu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Lys | Phe | Glu | Gly | Asp | Thr | Leu | Val | Asn | Arg | Ile | Glu | Leu | Lys | Gly |
| | | | 115 | | | | 120 | | | | | 125 | | | |
| Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu | Gly | His | Lys | Leu | Glu | Tyr |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Asn | Tyr | Asn | Ser | His | Asn | Val | Tyr | Ile | Met | Ala | Asp | Lys | Gln | Lys | Asn |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Gly | Ile | Lys | Val | Asn | Phe | Lys | Thr | Arg | His | Asn | Ile | Glu | Asp | Gly | Ser |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn | Thr | Pro | Ile | Gly | Asp | Gly |
| | | | 180 | | | | | 185 | | | | | 190 | | |
| Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | Thr | Gln | Ser | Ala | Leu |
| | | | 195 | | | | 200 | | | | | 205 | | | |
| Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu | Leu | Glu | Phe |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Val | Thr | Ala | Ala | Gly | Ile | Thr | His | Gly | Met | Asp | Glu | Leu | Tyr | Asn | Thr |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Gly | Met | Leu | Ala | Arg | Arg | Lys | Pro | Val | Leu | Pro | Ala | Leu | Thr | Ile | Asn |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Pro | Thr | Ile | Ala | Glu | Gly | Pro | Ser | Pro | Thr | Ser | Glu | Gly | Ala | Ser | Glu |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Ala | Asn | Leu | Val | Asp | Leu | Gln | Lys | Lys | Leu | Glu | Glu | Leu | Glu | Leu | Asp |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Glu | Gln | Gln | | | | | | | | | | | | | |
| | | 290 | | | | | | | | | | | | | |

<210> 11
 <211> 889
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(888)

<220>

<223> Description of Artificial Sequence: Caspase
3-DEVD-substrate construct

<400> 11

| | |
|---|-----|
| atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt | 48 |
| Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu | |
| 1 5 10 15 | |
| ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga | 96 |
| Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly | |
| 20 25 30 | |
| gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc | 144 |
| Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile | |
| 35 40 45 | |
| tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act | 192 |
| Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr | |
| 50 55 60 | |
| ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa | 240 |
| Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys | |
| 65 70 75 80 | |
| cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa | 288 |
| Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu | |
| 85 90 95 | |
| agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa | 336 |
| Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu | |
| 100 105 110 | |
| gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt | 384 |
| Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly | |
| 115 120 125 | |
| att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac | 432 |
| Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr | |
| 130 135 140 | |
| aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat | 480 |
| Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn | |
| 145 150 155 160 | |
| gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc | 528 |
| Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser | |
| 165 170 175 | |
| gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc | 576 |
| Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly | |
| 180 185 190 | |
| cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt | 624 |
| Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu | |
| 195 200 205 | |

| | |
|---|-----|
| tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt | 672 |
| Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe | |
| 210 215 220 | |
| | |
| gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc | 720 |
| Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser | |
| 225 230 235 240 | |
| | |
| gga aga agg aaa cga caa aag cga tcg gct gtt aaa tct gaa gga aag | 768 |
| Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Val Lys Ser Glu Gly Lys | |
| 245 250 255 | |
| | |
| aga aag tgt gac gaa gtt gat gga att gat gaa gta gca agt act atg | 816 |
| Arg Lys Cys Asp Glu Val Asp Gly Ile Asp Glu Val Ala Ser Thr Met | |
| 260 265 270 | |
| | |
| tct act gtc cac gaa atc ctg tgc aag ctc agc ttg gag ggt gtt cat | 864 |
| Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His | |
| 275 280 285 | |
| | |
| tct aca ccc cca agt acc cgg atc c | 889 |
| Ser Thr Pro Pro Ser Thr Arg Ile | |
| 290 295 | |

<210> 12
 <211> 296
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Caspase
 3-DEVD-substrate construct

<400> 12

| | |
|---|--|
| Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu | |
| 1 5 10 15 | |
| | |
| Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly | |
| 20 25 30 | |
| | |
| Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile | |
| 35 40 45 | |
| | |
| Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr | |
| 50 55 60 | |
| | |
| Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys | |
| 65 70 75 80 | |
| | |
| Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu | |
| 85 90 95 | |
| | |
| Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu | |
| 100 105 110 | |
| | |
| Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly | |

bl

| 115 | | | | | 120 | | | | | 125 | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu | Gly | His | Lys | Leu | Glu | Tyr | | |
| 130 | | | | | 135 | | | | | 140 | | | | | | | |
| Asn | Tyr | Asn | Ser | His | Asn | Val | Tyr | Ile | Met | Ala | Asp | Lys | Gln | Lys | Asn | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| Gly | Ile | Lys | Val | Asn | Phe | Lys | Thr | Arg | His | Asn | Ile | Glu | Asp | Gly | Ser | | |
| 165 | | | | | 170 | | | | | 175 | | | | | | | |
| Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn | Thr | Pro | Ile | Gly | Asp | Gly | | |
| 180 | | | | | 185 | | | | | 190 | | | | | | | |
| Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | Thr | Gln | Ser | Ala | Leu | | |
| 195 | | | | | 200 | | | | | 205 | | | | | | | |
| Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu | Leu | Glu | Phe | | |
| 210 | | | | | 215 | | | | | 220 | | | | | | | |
| Val | Thr | Ala | Ala | Gly | Ile | Thr | His | Gly | Met | Asp | Glu | Leu | Tyr | Asn | Ser | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| Gly | Arg | Arg | Lys | Arg | Gln | Lys | Arg | Ser | Ala | Val | Lys | Ser | Glu | Gly | Lys | | |
| 245 | | | | | 250 | | | | | 255 | | | | | | | |
| Arg | Lys | Cys | Asp | Glu | Val | Asp | Gly | Ile | Asp | Glu | Val | Ala | Ser | Thr | Met | | |
| 260 | | | | | 265 | | | | | 270 | | | | | | | |
| Ser | Thr | Val | His | Glu | Ile | Leu | Cys | Lys | Leu | Ser | Leu | Glu | Gly | Val | His | | |
| 275 | | | | | 280 | | | | | 285 | | | | | | | |
| Ser | Thr | Pro | Pro | Ser | Thr | Arg | Ile | | | | | | | | | | |
| 290 | | | | | 295 | | | | | | | | | | | | |

<210> 13
 <211> 846
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(846)

<220>
 <223> Description of Artificial Sequence: Caspase
 6-VEID-substrate construct

<400> 13
 atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc 528
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc 720
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240

gga aga agg aaa cga caa aag cga tcg aca aga ctt gtt gaa att gac 768
 Gly Arg Arg Lys Arg Gln Lys Arg Ser Thr Arg Leu Val Glu Ile Asp
 245 250 255

aac agt act atg agc aca gta cac gaa att tta tgt aaa tta agc tta 816
 Asn Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu
 260 265 270

gaa gga gta cac agt aca cca cca agc gca 846
 Glu Gly Val His Ser Thr Pro Pro Ser Ala
 275 280

<210> 14
 <211> 282
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Caspase
 6-VEID-substrate construct

<400> 14
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205

B1

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240

Gly Arg Arg Lys Arg Gln Lys Arg Ser Thr Arg Leu Val Glu Ile Asp
 245 250 255

Asn Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu
 260 265 270

Glu Gly Val His Ser Thr Pro Pro Ser Ala
 275 280

<210> 15
 <211> 876
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(876)

<220>
 <223> Description of Artificial Sequence: Caspase 8-VETD
 construct

<400> 15
 atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15

ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu

| 100 | 105 | 110 | |
|---|-----|-----|-----|
| gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly 115 120 125 | | | 384 |
| att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr 130 135 140 | | | 432 |
| aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn 145 150 155 160 | | | 480 |
| gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser 165 170 175 | | | 528 |
| gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly 180 185 190 | | | 576 |
| cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu 195 200 205 | | | 624 |
| tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe 210 215 220 | | | 672 |
| gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser 225 230 235 240 | | | 720 |
| gga aga agc aaa cga caa aag cga tcg tat gaa aaa gga ata cca gtt Gly Arg Ser Lys Arg Gln Lys Arg Ser Tyr Glu Lys Gly Ile Pro Val 245 250 255 | | | 768 |
| gaa aca gac agc gaa gag caa gct tat agt act atg tct act gtc cac Glu Thr Asp Ser Glu Glu Gln Ala Tyr Ser Thr Met Ser Thr Val His 260 265 270 | | | 816 |
| gaa atc ctg tgc aag ctc agc ttg gag ggt gtt cat tct aca ccc cca Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His Ser Thr Pro Pro 275 280 285 | | | 864 |
| agt gcc gga tcc Ser Ala Gly Ser 290 | | | 876 |

<210> 16

<211> 292

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase 8-VETD
construct

<400> 16

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
225 230 235 240

Gly Arg Ser Lys Arg Gln Lys Arg Ser Tyr Glu Lys Gly Ile Pro Val
245 250 255

Glu Thr Asp Ser Glu Glu Gln Ala Tyr Ser Thr Met Ser Thr Val His
260 265 270

Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His Ser Thr Pro Pro
275 280 285

Ser Ala Gly Ser
290

<210> 17
<211> 906
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(906)

<220>
<223> Description of Artificial Sequence: Cas 3-multiple
DEV D construct

<400> 17
atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80
cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat 480
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn

| 145 | 150 | 155 | 160 | |
|---|-----|-----|-----|-----|
| gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc | | | | 528 |
| Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser | 165 | 170 | 175 | |
| ggt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc | | | | 576 |
| Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly | 180 | 185 | 190 | |
| cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt | | | | 624 |
| Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu | 195 | 200 | 205 | |
| tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt | | | | 672 |
| Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe | 210 | 215 | 220 | |
| gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc | | | | 720 |
| Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser | 225 | 230 | 235 | 240 |
| gga aga agg aaa cga caa aag cga tcg gca ggt gac gaa gtt gat gca | | | | 768 |
| Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Gly Asp Glu Val Asp Ala | 245 | 250 | 255 | |
| ggt gac gaa gtt gat gca ggt gac gaa gtt gat gca ggt gac gaa gtt | | | | 816 |
| Gly Asp Glu Val Asp Ala Gly Asp Glu Val Asp Ala Gly Asp Glu Val | 260 | 265 | 270 | |
| gac gca ggt agt act atg tct act gtc cac gaa atc ctg tgc aag ctc | | | | 864 |
| Asp Ala Gly Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu | 275 | 280 | 285 | |
| agc ttg gag ggt gtt cat tct aca ccc cca agt gcc gga tcc | | | | 906 |
| Ser Leu Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser | 290 | 295 | 300 | |

<210> 18

<211> 302

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cas 3-multiple
DEVD construct

<400> 18

Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240
 Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Gly Asp Glu Val Asp Ala
 245 250 255
 Gly Asp Glu Val Asp Ala Gly Asp Glu Val Asp Ala Gly Asp Glu Val
 260 265 270
 Asp Ala Gly Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu
 275 280 285
 Ser Leu Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser
 290 295 300

<210> 19
 <211> 906
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS

<222> (1)..(885)

<220>

<223> Description of Artificial Sequence: Caspase
8-multiple VETD construct

<400> 19

| | |
|---|-----|
| atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt | 48 |
| Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu | |
| 1 5 10 15 | |
| ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga | 96 |
| Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly | |
| 20 25 30 | |
| gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc | 144 |
| Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile | |
| 35 40 45 | |
| tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act | 192 |
| Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr | |
| 50 55 60 | |
| ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa | 240 |
| Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys | |
| 65 70 75 80 | |
| cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa | 288 |
| Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu | |
| 85 90 95 | |
| agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa | 336 |
| Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu | |
| 100 105 110 | |
| gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt | 384 |
| Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly | |
| 115 120 125 | |
| att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac | 432 |
| Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr | |
| 130 135 140 | |
| aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat | 480 |
| Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn | |
| 145 150 155 160 | |
| gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc | 528 |
| Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser | |
| 165 170 175 | |
| ggt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc | 576 |
| Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly | |
| 180 185 190 | |
| cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt | 624 |
| Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu | |

| 195 | 200 | 205 | |
|---|-----|-----|-----|
| tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt | | | 672 |
| Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe | | | |
| 210 | 215 | 220 | |
| gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc | | | 720 |
| Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser | | | |
| 225 | 230 | 235 | 240 |
| gga aga agg aaa cga caa aag cga tcg gca ggt gtt gaa aca gac gca | | | 768 |
| Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Gly Val Glu Thr Asp Ala | | | |
| 245 | 250 | 255 | |
| ggt gtt gaa aca gac gca ggt gtt gaa aca gac gca ggt gtt gaa aca | | | 816 |
| Gly Val Glu Thr Asp Ala Gly Val Glu Thr Asp Ala Gly Val Glu Thr | | | |
| 260 | 265 | 270 | |
| gac gca ggt agt act atg tct act gtc cac gaa atc ctg tgc aag ctc | | | 864 |
| Asp Ala Gly Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu | | | |
| 275 | 280 | 285 | |
| agc ttg gag ggt gtt cat tct acacccccaa gtgccggatc c | | | 906 |
| Ser Leu Glu Gly Val His Ser | | | |
| 290 | 295 | | |

<210> 20

<211> 295

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase
8-multiple VETD construct

<400> 20

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Ala | Ser | Lys | Gly | Glu | Glu | Leu | Phe | Thr | Gly | Val | Val | Pro | Ile | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Glu | Leu | Asp | Gly | Asp | Val | Asn | Gly | His | Lys | Phe | Ser | Val | Ser | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Gly | Glu | Gly | Asp | Ala | Thr | Tyr | Gly | Lys | Leu | Thr | Leu | Lys | Phe | Ile |
| | | | 35 | | | | | 40 | | | | | 45 | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Cys | Thr | Thr | Gly | Lys | Leu | Pro | Val | Pro | Trp | Pro | Thr | Leu | Val | Thr | Thr |
| | 50 | | | | | 55 | | | | | 60 | | | | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Cys | Tyr | Gly | Val | Gln | Cys | Phe | Ser | Arg | Tyr | Pro | Asp | His | Met | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | 80 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro | Glu | Gly | Tyr | Val | Gln | Glu |
| | | | | 85 | | | | 90 | | | | | | 95 | |

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn | Tyr | Lys | Thr | Arg | Ala | Glu |
| | | | 100 | | | | | 105 | | | | | 110 | | |

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
 225 230 235 240
 Gly Arg Arg Lys Arg Gln Lys Arg Ser Ala Gly Val Glu Thr Asp Ala
 245 250 255
 Gly Val Glu Thr Asp Ala Gly Val Glu Thr Asp Ala Gly Val Glu Thr
 260 265 270
 Asp Ala Gly Ser Thr Met Ser Thr Val His Glu Ile Leu Cys Lys Leu
 275 280 285
 Ser Leu Glu Gly Val His Ser
 290 295

<210> 21
 <211> 4833
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1) .. (4830)

<220>
 <223> Description of Artificial Sequence:
 EYFP-DEVD-MAP4-EBFP construct

<400> 21
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Val | Glu | Leu | Asp | Gly | Asp | Val | Asn | Gly | His | Lys | Phe | Ser | Val | Ser | Gly | | |
| | | | 20 | | | | | 25 | | | | | 30 | | | | |
| gag | ggc | gag | ggc | gat | gcc | acc | tac | ggc | aag | ctg | acc | ctg | aag | ttc | atc | 144 | |
| Glu | Gly | Glu | Gly | Asp | Ala | Thr | Tyr | Gly | Lys | Leu | Thr | Leu | Lys | Phe | Ile | | |
| | | 35 | | | | | 40 | | | | | 45 | | | | | |
| tgc | acc | acc | ggc | aag | ctg | ccc | gtg | ccc | tgg | ccc | acc | ctc | gtg | acc | acc | 192 | |
| Cys | Thr | Thr | Gly | Lys | Leu | Pro | Val | Pro | Trp | Pro | Thr | Leu | Val | Thr | Thr | | |
| | 50 | | | | | 55 | | | | | 60 | | | | | | |
| ttc | ggc | tac | ggc | ctg | cag | tgc | ttc | gcc | cgc | tac | ccc | gac | cac | atg | aag | 240 | |
| Phe | Gly | Tyr | Gly | Leu | Gln | Cys | Phe | Ala | Arg | Tyr | Pro | Asp | His | Met | Lys | | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | | |
| cag | cac | gac | ttc | ttc | aag | tcc | gcc | atg | ccc | gaa | ggc | tac | gtc | cag | gag | 288 | |
| Gln | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro | Glu | Gly | Tyr | Val | Gln | Glu | | |
| | | | 85 | | | | | | 90 | | | | | 95 | | | |
| cgc | acc | atc | ttc | ttc | aag | gac | gac | ggc | aac | tac | aag | acc | cgc | gcc | gag | 336 | |
| Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn | Tyr | Lys | Thr | Arg | Ala | Glu | | |
| | | 100 | | | | | | 105 | | | | | 110 | | | | |
| gtg | aag | ttc | gag | ggc | gac | acc | ctg | gtg | aac | cgc | atc | gag | ctg | aag | ggc | 384 | |
| Val | Lys | Phe | Glu | Gly | Asp | Thr | Leu | Val | Asn | Arg | Ile | Glu | Leu | Lys | Gly | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| atc | gac | ttc | aag | gag | gac | ggc | aac | atc | ctg | ggg | cac | aag | ctg | gag | tac | 432 | |
| Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu | Gly | His | Lys | Leu | Glu | Tyr | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |
| aac | tac | aac | agc | cac | aac | gtc | tat | atc | atg | gcc | gac | aag | cag | aag | aac | 480 | |
| Asn | Tyr | Asn | Ser | His | Asn | Val | Tyr | Ile | Met | Ala | Asp | Lys | Gln | Lys | Asn | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| ggc | atc | aag | gtg | aac | ttc | aag | atc | cgc | cac | aac | atc | gag | gac | ggc | agc | 528 | |
| Gly | Ile | Lys | Val | Asn | Phe | Lys | Ile | Arg | His | Asn | Ile | Glu | Asp | Gly | Ser | | |
| | | | 165 | | | | | 170 | | | | | | 175 | | | |
| gtg | cag | ctc | gcc | gac | cac | tac | cag | cag | aac | acc | ccc | atc | ggc | gac | ggc | 576 | |
| Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn | Thr | Pro | Ile | Gly | Asp | Gly | | |
| | | 180 | | | | | 185 | | | | | | 190 | | | | |
| ccc | gtg | ctg | ctg | ccc | gac | aac | cac | tac | ctg | agc | tac | cag | tcc | gcc | ctg | 624 | |
| Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | Tyr | Gln | Ser | Ala | Leu | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| agc | aaa | gac | ccc | aac | gag | aag | cgc | gat | cac | atg | gtc | ctg | ctg | gag | ttc | 672 | |
| Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu | Leu | Glu | Phe | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| gtg | acc | gcc | gcc | ggg | atc | act | ctc | ggc | atg | gac | gag | ctg | tac | aag | aag | 720 | |
| Val | Thr | Ala | Ala | Gly | Ile | Thr | Leu | Gly | Met | Asp | Glu | Leu | Tyr | Lys | Lys | | |
| | 225 | | | | 230 | | | | 235 | | | | | | 240 | | |
| gga | gac | gaa | gtg | gac | gga | atg | gcc | gac | ctc | agt | ctt | gtg | gat | gcg | ttg | 768 | |
| Gly | Asp | Glu | Val | Asp | Gly | Met | Ala | Asp | Leu | Ser | Leu | Val | Asp | Ala | Leu | | |

| 245 | | | | | | | | | | 250 | | | | | | | | | | 255 | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|--|--|-----|--|--|--|--|--|--|--|--|--|--|
| aca | gaa | cca | cct | cca | gaa | att | gag | gga | gaa | ata | aag | cga | gac | ttc | atg | 816 | | | | | | | | | | | | | | |
| Thr | Glu | Pro | Pro | Pro | Glu | Ile | Glu | Gly | Glu | Ile | Lys | Arg | Asp | Phe | Met | | | | | | | | | | | | | | | |
| 260 | | | | | 265 | | | | | 270 | | | | | | | | | | | | | | | | | | | | |
| gct | gcg | ctg | gag | gca | gag | ccc | tat | gat | gac | atc | gtg | gga | gaa | act | gtg | 864 | | | | | | | | | | | | | | |
| Ala | Ala | Leu | Glu | Ala | Glu | Pro | Tyr | Asp | Asp | Ile | Val | Gly | Glu | Thr | Val | | | | | | | | | | | | | | | |
| 275 | | | | | 280 | | | | | 285 | | | | | | | | | | | | | | | | | | | | |
| gag | aaa | act | gag | ttt | att | cct | ctc | ctg | gat | ggg | gat | gag | aaa | acc | ggg | 912 | | | | | | | | | | | | | | |
| Glu | Lys | Thr | Glu | Phe | Ile | Pro | Leu | Leu | Asp | Gly | Asp | Glu | Lys | Thr | Gly | | | | | | | | | | | | | | | |
| 290 | | | | | 295 | | | | | 300 | | | | | | | | | | | | | | | | | | | | |
| aac | tca | gag | tcc | aaa | aag | aaa | ccc | tgc | tta | gac | act | agc | cag | gtt | gaa | 960 | | | | | | | | | | | | | | |
| Asn | Ser | Glu | Ser | Lys | Lys | Lys | Pro | Cys | Leu | Asp | Thr | Ser | Gln | Val | Glu | | | | | | | | | | | | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | | | | | | | | | | | | | | | |
| ggg | atc | cca | tct | tct | aaa | cca | aca | ctc | cta | gcc | aat | ggg | gat | cat | gga | 1008 | | | | | | | | | | | | | | |
| Gly | Ile | Pro | Ser | Ser | Lys | Pro | Thr | Leu | Leu | Ala | Asn | Gly | Asp | His | Gly | | | | | | | | | | | | | | | |
| 325 | | | | | 330 | | | | | 335 | | | | | | | | | | | | | | | | | | | | |
| atg | gag | ggg | aat | aac | act | gca | ggg | tct | cca | act | gac | ttc | ctt | gaa | gag | 1056 | | | | | | | | | | | | | | |
| Met | Glu | Gly | Asn | Asn | Thr | Ala | Gly | Ser | Pro | Thr | Asp | Phe | Leu | Glu | Glu | | | | | | | | | | | | | | | |
| 340 | | | | | 345 | | | | | 350 | | | | | | | | | | | | | | | | | | | | |
| aga | gtg | gac | tat | ccg | gat | tat | cag | agc | agc | cag | aac | tgg | cca | gaa | gat | 1104 | | | | | | | | | | | | | | |
| Arg | Val | Asp | Tyr | Pro | Asp | Tyr | Gln | Ser | Ser | Gln | Asn | Trp | Pro | Glu | Asp | | | | | | | | | | | | | | | |
| 355 | | | | | 360 | | | | | 365 | | | | | | | | | | | | | | | | | | | | |
| gca | agc | ttt | tgt | ttc | cag | cct | cag | caa | gtg | tta | gat | act | gac | cag | gct | 1152 | | | | | | | | | | | | | | |
| Ala | Ser | Phe | Cys | Phe | Gln | Pro | Gln | Gln | Val | Leu | Asp | Thr | Asp | Gln | Ala | | | | | | | | | | | | | | | |
| 370 | | | | | 375 | | | | | 380 | | | | | | | | | | | | | | | | | | | | |
| gag | ccc | ttt | aac | gag | cac | cgt | gat | gat | ggg | ttg | gca | gat | ctg | ctc | ttt | 1200 | | | | | | | | | | | | | | |
| Glu | Pro | Phe | Asn | Glu | His | Arg | Asp | Asp | Gly | Leu | Ala | Asp | Leu | Leu | Phe | | | | | | | | | | | | | | | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | | | | | | | | | | | | | | | |
| gtc | tcc | agt | gga | ccc | acg | aac | gct | tct | gca | ttt | aca | gag | cga | gac | aat | 1248 | | | | | | | | | | | | | | |
| Val | Ser | Ser | Gly | Pro | Thr | Asn | Ala | Ser | Ala | Phe | Thr | Glu | Arg | Asp | Asn | | | | | | | | | | | | | | | |
| 405 | | | | | 410 | | | | | 415 | | | | | | | | | | | | | | | | | | | | |
| cct | tca | gaa | gac | agt | tac | ggg | atg | ctt | ccc | tgt | gac | tca | ttt | gct | tcc | 1296 | | | | | | | | | | | | | | |
| Pro | Ser | Glu | Asp | Ser | Tyr | Gly | Met | Leu | Pro | Cys | Asp | Ser | Phe | Ala | Ser | | | | | | | | | | | | | | | |
| 420 | | | | | 425 | | | | | 430 | | | | | | | | | | | | | | | | | | | | |
| acg | gct | gtt | gta | tct | cag | gag | tgg | tct | gtg | gga | gcc | cca | aac | tct | cca | 1344 | | | | | | | | | | | | | | |
| Thr | Ala | Val | Val | Ser | Gln | Glu | Trp | Ser | Val | Gly | Ala | Pro | Asn | Ser | Pro | | | | | | | | | | | | | | | |
| 435 | | | | | 440 | | | | | 445 | | | | | | | | | | | | | | | | | | | | |
| tgt | tca | gag | tcc | tgt | gtc | tcc | cca | gag | gtt | act | ata | gaa | acc | cta | cag | 1392 | | | | | | | | | | | | | | |
| Cys | Ser | Glu | Ser | Cys | Val | Ser | Pro | Glu | Val | Thr | Ile | Glu | Thr | Leu | Gln | | | | | | | | | | | | | | | |
| 450 | | | | | 455 | | | | | 460 | | | | | | | | | | | | | | | | | | | | |
| cca | gca | aca | gag | ctc | tcc | aag | gca | gca | gaa | gtg | gaa | tca | gtg | aaa | gag | 1440 | | | | | | | | | | | | | | |
| Pro | Ala | Thr | Glu | Leu | Ser | Lys | Ala | Ala | Glu | Val | Glu | Ser | Val | Lys | Glu | | | | | | | | | | | | | | | |
| 465 | | | | | 470 | | | | | 475 | | | | | 480 | | | | | | | | | | | | | | | |

bl

| | |
|---|------|
| cag ctg cca gct aaa gca ttg gaa acg atg gca gag cag acc act gat | 1488 |
| Gln Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp | |
| 485 490 495 | |
| gtg gtg cac tct cca tcc aca gac aca aca cca ggc cca gac aca gag | 1536 |
| Val Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu | |
| 500 505 510 | |
| gca gca ctg gct aaa gac ata gaa gag atc acc aag cca gat gtg ata | 1584 |
| Ala Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile | |
| 515 520 525 | |
| ttg gca aat gtc acg cag cca tct act gaa tcg gat atg ttc ctg gcc | 1632 |
| Leu Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala | |
| 530 535 540 | |
| cag gac atg gaa cta ctc aca gga aca gag gca gcc cac gct aac aat | 1680 |
| Gln Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn | |
| 545 550 555 560 | |
| atc ata ttg cct aca gaa cca gac gaa tct tca acc aag gat gta gca | 1728 |
| Ile Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr Lys Asp Val Ala | |
| 565 570 575 | |
| cca cct atg gaa gaa gaa att gtc cca ggc aat gat acg aca tcc ccc | 1776 |
| Pro Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp Thr Thr Ser Pro | |
| 580 585 590 | |
| aaa gaa aca gag aca aca ctt cca ata aaa atg gac ttg gca cca cct | 1824 |
| Lys Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp Leu Ala Pro Pro | |
| 595 600 605 | |
| gag gat gtg tta ctt acc aaa gaa aca gaa cta gcc cca gcc aag ggc | 1872 |
| Glu Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly | |
| 610 615 620 | |
| atg gtt tca ctc tca gaa ata gaa gag gct ctg gca aag aat gat gtt | 1920 |
| Met Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala Lys Asn Asp Val | |
| 625 630 635 640 | |
| cgc tct gca gaa ata cct gtg gct cag gag aca gtg gtc tca gaa aca | 1968 |
| Arg Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val Val Ser Glu Thr | |
| 645 650 655 | |
| gag gtg gtc ctg gca aca gaa gtg gta ctg ccc tca gat ccc ata aca | 2016 |
| Glu Val Val Leu Ala Thr Glu Val Val Leu Pro Ser Asp Pro Ile Thr | |
| 660 665 670 | |
| aca ttg aca aag gat gtg aca ctc ccc tta gaa gca gag aga ccg ttg | 2064 |
| Thr Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu | |
| 675 680 685 | |
| gtg acg gac atg act cca tct ctg gaa aca gaa atg acc cta ggc aaa | 2112 |
| Val Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met Thr Leu Gly Lys | |
| 690 695 700 | |

B1

| | |
|---|------|
| gag aca gct cca ccc aca gaa aca aat ttg ggc atg gcc aaa gac atg | 2160 |
| Glu Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met Ala Lys Asp Met | |
| 705 710 715 720 | |
| tct cca ctc cca gaa tca gaa gtg act ctg ggc aag gac gtg gtt ata | 2208 |
| Ser Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys Asp Val Val Ile | |
| 725 730 735 | |
| ctt cca gaa aca aag gtg gct gag ttt aac aat gtg act cca ctt tca | 2256 |
| Leu Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val Thr Pro Leu Ser | |
| 740 745 750 | |
| gaa gaa gag gta acc tca gtc aag gac atg tct ccg tct gca gaa aca | 2304 |
| Glu Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro Ser Ala Glu Thr | |
| 755 760 765 | |
| gag gct ccc ctg gct aag aat gct gat ctg cac tca gga aca gag ctg | 2352 |
| Glu Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser Gly Thr Glu Leu | |
| 770 775 780 | |
| att gtg gac aac agc atg gct cca gcc tcc gat ctt gca ctg ccc ttg | 2400 |
| Ile Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu | |
| 785 790 795 800 | |
| gaa aca aaa gta gca aca gtt cca att aaa gac aaa gga act gta cag | 2448 |
| Glu Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys Gly Thr Val Gln | |
| 805 810 815 | |
| act gaa gaa aaa cca cgt gaa gac tcc cag tta gca tct atg cag cac | 2496 |
| Thr Glu Glu Lys Pro Arg Glu Asp Ser Gln Leu Ala Ser Met Gln His | |
| 820 825 830 | |
| aag gga cag tca aca gta cct cct tgc acg gct tca cca gaa cca gtc | 2544 |
| Lys Gly Gln Ser Thr Val Pro Pro Cys Thr Ala Ser Pro Glu Pro Val | |
| 835 840 845 | |
| aaa gct gca gaa caa atg tct acc tta cca ata gat gca cct tct cca | 2592 |
| Lys Ala Ala Glu Gln Met Ser Thr Leu Pro Ile Asp Ala Pro Ser Pro | |
| 850 855 860 | |
| tta gag aac tta gag cag aag gaa acg cct ggc agc cag cct tct gag | 2640 |
| Leu Glu Asn Leu Glu Gln Lys Glu Thr Pro Gly Ser Gln Pro Ser Glu | |
| 865 870 875 880 | |
| cct tgc tca gga gta tcc cgg caa gaa gaa gca aag gct gct gta ggt | 2688 |
| Pro Cys Ser Gly Val Ser Arg Gln Glu Glu Ala Lys Ala Ala Val Gly | |
| 885 890 895 | |
| gtg act gga aat gac atc act acc ccg cca aac aag gag cca cca cca | 2736 |
| Val Thr Gly Asn Asp Ile Thr Thr Pro Pro Asn Lys Glu Pro Pro Pro | |
| 900 905 910 | |
| agc cca gaa aag aaa gca aag cct ttg gcc acc act caa cct gca aag | 2784 |
| Ser Pro Glu Lys Lys Ala Lys Pro Leu Ala Thr Thr Gln Pro Ala Lys | |
| 915 920 925 | |
| act tca aca tcg aaa gcc aaa aca cag ccc act tct ctc cct aag caa | 2832 |

B1

| | | | | | | | | | | | | | | | | | |
|------|------|------|------|------|------|------|------|------|------|------|------|------|------|------|-----|------|--|
| Thr | Ser | Thr | Ser | Lys | Ala | Lys | Thr | Gln | Pro | Thr | Ser | Leu | Pro | Lys | Gln | | |
| 930 | | | | | | 935 | | | | | 940 | | | | | | |
| cca | gct | ccc | acc | acc | tct | ggg | ggg | ttg | aat | aaa | aaa | ccc | atg | agc | ctc | 2880 | |
| Pro | Ala | Pro | Thr | Thr | Ser | Gly | Gly | Leu | Asn | Lys | Lys | Pro | Met | Ser | Leu | | |
| 945 | | | | | 950 | | | | 955 | | | | | | 960 | | |
| gcc | tca | ggc | tca | gtg | cca | gct | gcc | cca | cac | aaa | cgc | cct | gct | gct | gcc | 2928 | |
| Ala | Ser | Gly | Ser | Val | Pro | Ala | Ala | Pro | His | Lys | Arg | Pro | Ala | Ala | Ala | | |
| | | | | 965 | | | | 970 | | | | | | 975 | | | |
| act | gct | act | gcc | agg | cct | tcc | acc | cta | cct | gcc | aga | gac | gtg | aag | cca | 2976 | |
| Thr | Ala | Thr | Ala | Arg | Pro | Ser | Thr | Leu | Pro | Ala | Arg | Asp | Val | Lys | Pro | | |
| | | | 980 | | | | | 985 | | | | | 990 | | | | |
| aag | cca | att | aca | gaa | gct | aag | gtt | gcc | gaa | aag | cgg | acc | tct | cca | tcc | 3024 | |
| Lys | Pro | Ile | Thr | Glu | Ala | Lys | Val | Ala | Glu | Lys | Arg | Thr | Ser | Pro | Ser | | |
| | 995 | | | | | 1000 | | | | | 1005 | | | | | | |
| aag | cct | tca | tct | gcc | cca | gcc | ctc | aaa | cct | gga | cct | aaa | acc | acc | cca | 3072 | |
| Lys | Pro | Ser | Ser | Ala | Pro | Ala | Leu | Lys | Pro | Gly | Pro | Lys | Thr | Thr | Pro | | |
| | 1010 | | | | | 1015 | | | | 1020 | | | | | | | |
| acc | gtt | tca | aaa | gcc | aca | tct | ccc | tca | act | ctt | gtt | tcc | act | gga | cca | 3120 | |
| Thr | Val | Ser | Lys | Ala | Thr | Ser | Pro | Ser | Thr | Leu | Val | Ser | Thr | Gly | Pro | | |
| 1025 | | | | | 1030 | | | | 1035 | | | | | 1040 | | | |
| agt | agt | aga | agt | cca | gct | aca | act | ctg | cct | aag | agg | cca | acc | agc | atc | 3168 | |
| Ser | Ser | Arg | Ser | Pro | Ala | Thr | Thr | Leu | Pro | Lys | Arg | Pro | Thr | Ser | Ile | | |
| | | | | 1045 | | | | 1050 | | | | | | 1055 | | | |
| aag | act | gag | ggg | aaa | cct | gct | gat | gtc | aaa | agg | atg | act | gct | aag | tct | 3216 | |
| Lys | Thr | Glu | Gly | Lys | Pro | Ala | Asp | Val | Lys | Arg | Met | Thr | Ala | Lys | Ser | | |
| | | 1060 | | | | | | 1065 | | | | | 1070 | | | | |
| gcc | tca | gct | gac | ttg | agt | cgc | tca | aag | acc | acc | tct | gcc | agt | tct | gtg | 3264 | |
| Ala | Ser | Ala | Asp | Leu | Ser | Arg | Ser | Lys | Thr | Thr | Ser | Ala | Ser | Ser | Val | | |
| | | 1075 | | | | | 1080 | | | | | 1085 | | | | | |
| aag | aga | aac | acc | act | ccc | act | ggg | gca | gca | ccc | cca | gca | ggg | atg | act | 3312 | |
| Lys | Arg | Asn | Thr | Thr | Pro | Thr | Gly | Ala | Ala | Pro | Pro | Ala | Gly | Met | Thr | | |
| | 1090 | | | | | 1095 | | | | 1100 | | | | | | | |
| tcc | act | cga | gtc | aag | ccc | atg | tct | gca | cct | agc | cgc | tct | tct | ggg | gct | 3360 | |
| Ser | Thr | Arg | Val | Lys | Pro | Met | Ser | Ala | Pro | Ser | Arg | Ser | Ser | Gly | Ala | | |
| 1105 | | | | 1110 | | | | | 1115 | | | | | 1120 | | | |
| ctt | tct | gtg | gac | aag | aag | ccc | act | tcc | act | aag | cct | agc | tcc | tct | gct | 3408 | |
| Leu | Ser | Val | Asp | Lys | Lys | Pro | Thr | Ser | Thr | Lys | Pro | Ser | Ser | Ser | Ala | | |
| | | | 1125 | | | | | 1130 | | | | | 1135 | | | | |
| ccc | agg | gtg | agc | cgc | ctg | gcc | aca | act | gtt | tct | gcc | cct | gac | ctg | aag | 3456 | |
| Pro | Arg | Val | Ser | Arg | Leu | Ala | Thr | Thr | Val | Ser | Ala | Pro | Asp | Leu | Lys | | |
| | | 1140 | | | | | 1145 | | | | | 1150 | | | | | |
| agt | gtt | cgc | tcc | aag | gtc | ggc | tct | aca | gaa | aac | atc | aaa | cac | cag | cct | 3504 | |
| Ser | Val | Arg | Ser | Lys | Val | Gly | Ser | Thr | Glu | Asn | Ile | Lys | His | Gln | Pro | | |

| 1155 | 1160 | 1165 | |
|---|------|------|------|
| gga gga ggc cgg gcc aaa gta gag aaa aaa aca gag gca gct acc aca Gly Gly Gly Arg Ala Lys Val Glu Lys Lys Thr Glu Ala Ala Thr Thr 1170 1175 1180 | | | 3552 |
| gct ggg aag cct gaa cct aat gca gtc act aaa gca gcc ggc tcc att Ala Gly Lys Pro Glu Pro Asn Ala Val Thr Lys Ala Ala Gly Ser Ile 1185 1190 1195 1200 | | | 3600 |
| gcg agt gca cag aaa ccg cct gct ggg aaa gtc cag ata gta tcc aaa Ala Ser Ala Gln Lys Pro Pro Ala Gly Lys Val Gln Ile Val Ser Lys 1205 1210 1215 | | | 3648 |
| aaa gtg agc tac agt cat att caa tcc aag tgt gtt tcc aag gac aat Lys Val Ser Tyr Ser His Ile Gln Ser Lys Cys Val Ser Lys Asp Asn 1220 1225 1230 | | | 3696 |
| att aag cat gtc cct gga tgt ggc aat gtt cag att cag aac aag aaa Ile Lys His Val Pro Gly Cys Gly Asn Val Gln Ile Gln Asn Lys Lys 1235 1240 1245 | | | 3744 |
| gtg gac ata tcc aag gtc tcc tcc aag tgt ggg tcc aaa gct aat atc Val Asp Ile Ser Lys Val Ser Ser Lys Cys Gly Ser Lys Ala Asn Ile 1250 1255 1260 | | | 3792 |
| aag cac aag cct ggt gga gga gat gtc aag att gaa agt cag aag ttg Lys His Lys Pro Gly Gly Gly Asp Val Lys Ile Glu Ser Gln Lys Leu 1265 1270 1275 1280 | | | 3840 |
| aac ttc aag gag aag gcc caa gcc aaa gtg gga tcc ctt gat aac gtt Asn Phe Lys Glu Lys Ala Gln Ala Lys Val Gly Ser Leu Asp Asn Val 1285 1290 1295 | | | 3888 |
| ggc cac ttt cct gca gga ggt gcc gtg aag act gag ggc ggt ggc agt Gly His Phe Pro Ala Gly Gly Ala Val Lys Thr Glu Gly Gly Gly Ser 1300 1305 1310 | | | 3936 |
| gag gcc ctt ccg tgt cca ggc ccc ccc gct ggg gag gag cca gtc atc Glu Ala Leu Pro Cys Pro Gly Pro Pro Ala Gly Glu Glu Pro Val Ile 1315 1320 1325 | | | 3984 |
| cct gag gct gcg cct gac cgt ggc gcc cct act tca gcc agt ggc ctc Pro Glu Ala Ala Pro Asp Arg Gly Ala Pro Thr Ser Ala Ser Gly Leu 1330 1335 1340 | | | 4032 |
| agt ggc cac acc acc ctg tca ggg ggt ggt gac caa agg gag ccc cag Ser Gly His Thr Thr Leu Ser Gly Gly Gly Asp Gln Arg Glu Pro Gln 1345 1350 1355 1360 | | | 4080 |
| acc ttg gac agc cag atc cag gag aca agc atc atg gtg agc aag ggc Thr Leu Asp Ser Gln Ile Gln Glu Thr Ser Ile Met Val Ser Lys Gly 1365 1370 1375 | | | 4128 |
| gag gag ctg ttc acc ggg gtg gtg ccc atc ctg gtc gag ctg gac ggc Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly 1380 1385 1390 | | | 4176 |

gac gta aac ggc cac aag ttc agc gtg tcc ggc gag ggc gag ggc gat 4224
Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
1395 1400 1405

gcc acc tac ggc aag ctg acc ctg aag ttc atc tgc acc acc ggc aag 4272
Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
1410 1415 1420

ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc ctg acc cac ggc gtg 4320
Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val
1425 1430 1435 1440

cag tgc ttc agc cgc tac ccc gac cac atg aag cag cac gac ttc ttc 4368
Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
1445 1450 1455

aag tcc gcc atg ccc gaa ggc tac gtc cag gag cgc acc atc ttc ttc 4416
Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
1460 1465 1470

aag gac gac ggc aac tac aag acc cgc gcc gag gtg aag ttc gag ggc 4464
Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
1475 1480 1485

gac acc ctg gtg aac cgc atc gag ctg aag ggc atc gac ttc aag gag 4512
Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
1490 1495 1500

gac ggc aac atc ctg ggg cac aag ctg gag tac aac ttc aac agc cac 4560
Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His
1505 1510 1515 1520

aac gtc tat atc atg gcc gac aag cag aag aac ggc atc aag gtg aac 4608
Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn
1525 1530 1535

ttc aag atc cgc cac aac atc gag gac ggc agc gtg cag ctc gcc gac 4656
Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
1540 1545 1550

cac tac cag cag aac acc ccc atc ggc gac ggc ccc gtg ctg ctg ccc 4704
His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
1555 1560 1565

gac aac cac tac ctg agc acc cag tcc gcc ctg agc aaa gac ccc aac 4752
Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
1570 1575 1580

gag aag cgc gat cac atg gtc ctg ctg gag ttc gtg acc gcc gcc ggg 4800
Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
1585 1590 1595 1600

atc act ctc ggc atg gac gag ctg tac aag tag 4833
Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
1605 1610

<210> 22
 <211> 1610
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 EYFP-DEVD-MAP4-EBFP construct

<400> 22
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Lys
 225 230 235 240
 Gly Asp Glu Val Asp Gly Met Ala Asp Leu Ser Leu Val Asp Ala Leu

B1

245 250 255
 Thr Glu Pro Pro Pro Glu Ile Glu Gly Glu Ile Lys Arg Asp Phe Met
 260 265 270
 Ala Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val Gly Glu Thr Val
 275 280 285
 Glu Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly
 290 295 300
 Asn Ser Glu Ser Lys Lys Lys Pro Cys Leu Asp Thr Ser Gln Val Glu
 305 310 315 320
 Gly Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn Gly Asp His Gly
 325 330 335
 Met Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu
 340 345 350
 Arg Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp
 355 360 365
 Ala Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp Thr Asp Gln Ala
 370 375 380
 Glu Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe
 385 390 395 400
 Val Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn
 405 410 415
 Pro Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp Ser Phe Ala Ser
 420 425 430
 Thr Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala Pro Asn Ser Pro
 435 440 445
 Cys Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile Glu Thr Leu Gln
 450 455 460
 Pro Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu Ser Val Lys Glu
 465 470 475 480
 Gln Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu Gln Thr Thr Asp
 485 490 495
 Val Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu
 500 505 510
 Ala Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys Pro Asp Val Ile
 515 520 525
 Leu Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp Met Phe Leu Ala
 530 535 540
 Gln Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala His Ala Asn Asn

850 855 860
 Leu Glu Asn Leu Glu Gln Lys Glu Thr Pro Gly Ser Gln Pro Ser Glu
 865 870 875 880
 Pro Cys Ser Gly Val Ser Arg Gln Glu Glu Ala Lys Ala Ala Val Gly
 885 890 895
 Val Thr Gly Asn Asp Ile Thr Thr Pro Pro Asn Lys Glu Pro Pro Pro
 900 905 910
 Ser Pro Glu Lys Lys Ala Lys Pro Leu Ala Thr Thr Gln Pro Ala Lys
 915 920 925
 Thr Ser Thr Ser Lys Ala Lys Thr Gln Pro Thr Ser Leu Pro Lys Gln
 930 935 940
 Pro Ala Pro Thr Thr Ser Gly Gly Leu Asn Lys Lys Pro Met Ser Leu
 945 950 955 960
 Ala Ser Gly Ser Val Pro Ala Ala Pro His Lys Arg Pro Ala Ala Ala
 965 970 975
 Thr Ala Thr Ala Arg Pro Ser Thr Leu Pro Ala Arg Asp Val Lys Pro
 980 985 990
 Lys Pro Ile Thr Glu Ala Lys Val Ala Glu Lys Arg Thr Ser Pro Ser
 995 1000 1005
 Lys Pro Ser Ser Ala Pro Ala Leu Lys Pro Gly Pro Lys Thr Thr Pro
 1010 1015 1020
 Thr Val Ser Lys Ala Thr Ser Pro Ser Thr Leu Val Ser Thr Gly Pro
 1025 1030 1035 1040
 Ser Ser Arg Ser Pro Ala Thr Thr Leu Pro Lys Arg Pro Thr Ser Ile
 1045 1050 1055
 Lys Thr Glu Gly Lys Pro Ala Asp Val Lys Arg Met Thr Ala Lys Ser
 1060 1065 1070
 Ala Ser Ala Asp Leu Ser Arg Ser Lys Thr Thr Ser Ala Ser Ser Val
 1075 1080 1085
 Lys Arg Asn Thr Thr Pro Thr Gly Ala Ala Pro Pro Ala Gly Met Thr
 1090 1095 1100
 Ser Thr Arg Val Lys Pro Met Ser Ala Pro Ser Arg Ser Ser Gly Ala
 1105 1110 1115 1120
 Leu Ser Val Asp Lys Lys Pro Thr Ser Thr Lys Pro Ser Ser Ser Ala
 1125 1130 1135
 Pro Arg Val Ser Arg Leu Ala Thr Thr Val Ser Ala Pro Asp Leu Lys
 1140 1145 1150
 Ser Val Arg Ser Lys Val Gly Ser Thr Glu Asn Ile Lys His Gln Pro

| 1155 | 1160 | 1165 |
|--|------|------|
| Gly Gly Gly Arg Ala Lys Val Glu Lys Lys Thr Glu Ala Ala Thr Thr 1170 1175 1180 | | |
| Ala Gly Lys Pro Glu Pro Asn Ala Val Thr Lys Ala Ala Gly Ser Ile 1185 1190 1195 1200 | | |
| Ala Ser Ala Gln Lys Pro Pro Ala Gly Lys Val Gln Ile Val Ser Lys 1205 1210 1215 | | |
| Lys Val Ser Tyr Ser His Ile Gln Ser Lys Cys Val Ser Lys Asp Asn 1220 1225 1230 | | |
| Ile Lys His Val Pro Gly Cys Gly Asn Val Gln Ile Gln Asn Lys Lys 1235 1240 1245 | | |
| Val Asp Ile Ser Lys Val Ser Ser Lys Cys Gly Ser Lys Ala Asn Ile 1250 1255 1260 | | |
| Lys His Lys Pro Gly Gly Gly Asp Val Lys Ile Glu Ser Gln Lys Leu 1265 1270 1275 1280 | | |
| Asn Phe Lys Glu Lys Ala Gln Ala Lys Val Gly Ser Leu Asp Asn Val 1285 1290 1295 | | |
| Gly His Phe Pro Ala Gly Gly Ala Val Lys Thr Glu Gly Gly Gly Ser 1300 1305 1310 | | |
| Glu Ala Leu Pro Cys Pro Gly Pro Pro Ala Gly Glu Glu Pro Val Ile 1315 1320 1325 | | |
| Pro Glu Ala Ala Pro Asp Arg Gly Ala Pro Thr Ser Ala Ser Gly Leu 1330 1335 1340 | | |
| Ser Gly His Thr Thr Leu Ser Gly Gly Gly Asp Gln Arg Glu Pro Gln 1345 1350 1355 1360 | | |
| Thr Leu Asp Ser Gln Ile Gln Glu Thr Ser Ile Met Val Ser Lys Gly 1365 1370 1375 | | |
| Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly 1380 1385 1390 | | |
| Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp 1395 1400 1405 | | |
| Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys 1410 1415 1420 | | |
| Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr His Gly Val 1425 1430 1435 1440 | | |
| Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe 1445 1450 1455 | | |
| Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe | | |

| | | |
|---|------|------|
| 1460 | 1465 | 1470 |
| Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly | | |
| 1475 | 1480 | 1485 |
| Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu | | |
| 1490 | 1495 | 1500 |
| Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Phe Asn Ser His | | |
| 1505 | 1510 | 1515 |
| Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn | | |
| 1525 | 1530 | 1535 |
| Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp | | |
| 1540 | 1545 | 1550 |
| His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro | | |
| 1555 | 1560 | 1565 |
| Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn | | |
| 1570 | 1575 | 1580 |
| Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly | | |
| 1585 | 1590 | 1595 |
| Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys | | |
| 1605 | 1610 | |

<210> 23
 <211> 978
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(978)

<220>
 <223> Description of Artificial Sequence:
 GFP-nucleolus-Caspase 8-annexin II construct

<400> 23

| | |
|---|-----|
| atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt | 48 |
| Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu | |
| 1 5 10 15 | |
| ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga | 96 |
| Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly | |
| 20 25 30 | |
| gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc | 144 |
| Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile | |
| 35 40 45 | |
| tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act | 192 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Cys | Thr | Thr | Gly | Lys | Leu | Pro | Val | Pro | Trp | Pro | Thr | Leu | Val | Thr | Thr | | |
| 50 | | | | | | 55 | | | | | 60 | | | | | | |
| ctg | tgc | tat | ggg | gtt | caa | tgc | ttt | tca | aga | tac | ccg | gat | cat | atg | aaa | 240 | |
| Leu | Cys | Tyr | Gly | Val | Gln | Cys | Phe | Ser | Arg | Tyr | Pro | Asp | His | Met | Lys | | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | | |
| cgg | cat | gac | ttt | ttc | aag | agt | gcc | atg | ccc | gaa | ggg | tat | gta | cag | gaa | 288 | |
| Arg | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro | Glu | Gly | Tyr | Val | Gln | Glu | | |
| | | | | 85 | | | | | 90 | | | | | 95 | | | |
| agg | acc | atc | ttc | ttc | aaa | gat | gac | ggc | aac | tac | aag | aca | cgt | gct | gaa | 336 | |
| Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn | Tyr | Lys | Thr | Arg | Ala | Glu | | |
| | | | 100 | | | | | 105 | | | | | 110 | | | | |
| gtc | aag | ttt | gaa | ggg | gat | acc | ctt | gtt | aat | aga | atc | gag | tta | aaa | ggg | 384 | |
| Val | Lys | Phe | Glu | Gly | Asp | Thr | Leu | Val | Asn | Arg | Ile | Glu | Leu | Lys | Gly | | |
| | | 115 | | | | | 120 | | | | | 125 | | | | | |
| att | gac | ttc | aag | gaa | gat | ggc | aac | att | ctg | gga | cac | aaa | ttg | gaa | tac | 432 | |
| Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu | Gly | His | Lys | Leu | Glu | Tyr | | |
| | 130 | | | | | 135 | | | | | 140 | | | | | | |
| aac | tat | aac | tca | cac | aat | gta | tac | atc | atg | gca | gac | aaa | caa | aag | aat | 480 | |
| Asn | Tyr | Asn | Ser | His | Asn | Val | Tyr | Ile | Met | Ala | Asp | Lys | Gln | Lys | Asn | | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | | |
| gga | atc | aaa | gtg | aac | ttc | aag | acc | cgc | cac | aac | att | gaa | gat | gga | agc | 528 | |
| Gly | Ile | Lys | Val | Asn | Phe | Lys | Thr | Arg | His | Asn | Ile | Glu | Asp | Gly | Ser | | |
| | | | 165 | | | | | 170 | | | | | | 175 | | | |
| gtt | caa | cta | gca | gac | cat | tat | caa | caa | aat | act | cca | att | ggc | gat | ggc | 576 | |
| Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn | Thr | Pro | Ile | Gly | Asp | Gly | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| cct | gtc | ctt | tta | cca | gac | aac | cat | tac | ctg | tcc | aca | caa | tct | gcc | ctt | 624 | |
| Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | Thr | Gln | Ser | Ala | Leu | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| tcg | aaa | gat | ccc | aac | gaa | aag | aga | gac | cac | atg | gtc | ctt | ctt | gag | ttt | 672 | |
| Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu | Leu | Glu | Phe | | |
| | 210 | | | | | 215 | | | | | 220 | | | | | | |
| gta | aca | gct | gct | ggg | att | aca | cat | ggc | atg | gat | gaa | ctg | tac | aac | tcc | 720 | |
| Val | Thr | Ala | Ala | Gly | Ile | Thr | His | Gly | Met | Asp | Glu | Leu | Tyr | Asn | Ser | | |
| 225 | | | | | 230 | | | | 235 | | | | | | 240 | | |
| gga | aga | aaa | cgt | ata | cgt | act | tac | ctc | aag | tcc | tgc | agg | cgg | atg | aaa | 768 | |
| Gly | Arg | Lys | Arg | Ile | Arg | Thr | Tyr | Leu | Lys | Ser | Cys | Arg | Arg | Met | Lys | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| aga | agt | ggg | ttt | gag | atg | tct | cga | cct | att | cct | tcc | cac | ctt | act | cga | 816 | |
| Arg | Ser | Gly | Phe | Glu | Met | Ser | Arg | Pro | Ile | Pro | Ser | His | Leu | Thr | Arg | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | |
| tcg | gca | ggg | gtt | gaa | aca | gac | gca | ggg | gtt | gaa | aca | gac | gca | ggg | gtt | 864 | |
| Ser | Ala | Gly | Val | Glu | Thr | Asp | Ala | Gly | Val | Glu | Thr | Asp | Ala | Gly | Val | | |

| 275 | 280 | 285 | |
|-------------------------|---------------------|---------------------|-----|
| gaa aca gac gca ggt gtt | gaa aca gac gca ggt | agt act atg tct act | 912 |
| Glu Thr Asp Ala Gly Val | Glu Thr Asp Ala Gly | Ser Thr Met Ser Thr | |
| 290 | 295 | 300 | |
| gtc cac gaa atc ctg tgc | aag ctc agc ttg gag | ggg gtt cat tct aca | 960 |
| Val His Glu Ile Leu Cys | Lys Leu Ser Leu Glu | Gly Val His Ser Thr | |
| 305 | 310 | 315 | 320 |
| ccc cca agt gcc gga tcc | | | 978 |
| Pro Pro Ser Ala Gly Ser | | | |
| 325 | | | |

<210> 24
 <211> 326
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 GFP-nucleolus-Caspase 8-annexin II construct

<400> 24
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser
225 230 235 240

Gly Arg Lys Arg Ile Arg Thr Tyr Leu Lys Ser Cys Arg Arg Met Lys
245 250 255

Arg Ser Gly Phe Glu Met Ser Arg Pro Ile Pro Ser His Leu Thr Arg
260 265 270

Ser Ala Gly Val Glu Thr Asp Ala Gly Val Glu Thr Asp Ala Gly Val
275 280 285

Glu Thr Asp Ala Gly Val Glu Thr Asp Ala Gly Ser Thr Met Ser Thr
290 295 300

Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val His Ser Thr
305 310 315 320

Pro Pro Ser Ala Gly Ser
325

<210> 25
<211> 948
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1) .. (948)

<220>
<223> Description of Artificial Sequence:
GFP-nucleolus-Caspase 3-annexin II construct

<400> 25
atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

ggt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

| | |
|---|-----|
| tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act | 192 |
| Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr | |
| 50 55 60 | |
| ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa | 240 |
| Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys | |
| 65 70 75 80 | |
| cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa | 288 |
| Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu | |
| 85 90 95 | |
| agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa | 336 |
| Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu | |
| 100 105 110 | |
| gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt | 384 |
| Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly | |
| 115 120 125 | |
| att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac | 432 |
| Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr | |
| 130 135 140 | |
| aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat | 480 |
| Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn | |
| 145 150 155 160 | |
| gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc | 528 |
| Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser | |
| 165 170 175 | |
| gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc | 576 |
| Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly | |
| 180 185 190 | |
| cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt | 624 |
| Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu | |
| 195 200 205 | |
| tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt | 672 |
| Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe | |
| 210 215 220 | |
| gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tcc | 720 |
| Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn Ser | |
| 225 230 235 240 | |
| gga aga aaa cgt ata cgt act tac ctc aag tcc tgc agg cgg atg aaa | 768 |
| Gly Arg Lys Arg Ile Arg Thr Tyr Leu Lys Ser Cys Arg Arg Met Lys | |
| 245 250 255 | |
| aga agt ggt ttt gag atg tct cga cct att cct tcc cac ctt act cga | 816 |
| Arg Ser Gly Phe Glu Met Ser Arg Pro Ile Pro Ser His Leu Thr Arg | |
| 260 265 270 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| tcg | tat | gaa | aaa | gga | ata | cca | gtt | gaa | aca | gac | agc | gaa | gag | caa | gct | 864 |
| Ser | Tyr | Glu | Lys | Gly | Ile | Pro | Val | Glu | Thr | Asp | Ser | Glu | Glu | Gln | Ala | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |

gag ggt gtt cat tct aca ccc cca agt gcc gga tcc 948
Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser
305 310 315

```
<220>
<223> Description of Artificial Sequence:
      GFP-nucleolus-Caspase 3-annexin II construct
```

Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly

| 180 | | | | | | | | | | 185 | | | | | 190 | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|--|--|--|
| Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | Thr | Gln | Ser | Ala | Leu | | | | | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | | | | | |
| Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu | Leu | Glu | Phe | | | | | | |
| | 210 | | | | | 215 | | | | 220 | | | | | | | | | | | |
| Val | Thr | Ala | Ala | Gly | Ile | Thr | His | Gly | Met | Asp | Glu | Leu | Tyr | Asn | Ser | | | | | | |
| 225 | | | | | 230 | | | | 235 | | | | | | 240 | | | | | | |
| Gly | Arg | Lys | Arg | Ile | Arg | Thr | Tyr | Leu | Lys | Ser | Cys | Arg | Arg | Met | Lys | | | | | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | | | | | |
| Arg | Ser | Gly | Phe | Glu | Met | Ser | Arg | Pro | Ile | Pro | Ser | His | Leu | Thr | Arg | | | | | | |
| | | 260 | | | | | | 265 | | | | | 270 | | | | | | | | |
| Ser | Tyr | Glu | Lys | Gly | Ile | Pro | Val | Glu | Thr | Asp | Ser | Glu | Glu | Gln | Ala | | | | | | |
| | 275 | | | | | 280 | | | | | | 285 | | | | | | | | | |
| Tyr | Ser | Thr | Met | Ser | Thr | Val | His | Glu | Ile | Leu | Cys | Lys | Leu | Ser | Leu | | | | | | |
| | 290 | | | | | 295 | | | | | 300 | | | | | | | | | | |
| Glu | Gly | Val | His | Ser | Thr | Pro | Pro | Ser | Ala | Gly | Ser | | | | | | | | | | |
| 305 | | | | | 310 | | | | | 315 | | | | | | | | | | | |

<210> 27
 <211> 2106
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1050)

<220>
 <223> Description of Artificial Sequence:
 NLS-Fred25-cellubrevin construct

<400> 27
 atg aga aga aaa cga caa aag gct agc aaa gga gaa gaa ctc ttc act 48
 Met Arg Arg Lys Arg Gln Lys Ala Ser Lys Gly Glu Glu Leu Phe Thr
 1 5 10 15

 gga gtt gtc cca att ctt gtt gaa tta gat ggt gat gtt aac ggc cac 96
 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 20 25 30

 aag ttc tct gtc agt gga gag ggt gaa ggt gat gca aca tac gga aaa 144
 Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
 35 40 45

 ctt acc ctg aag ttc atc tgc act act ggc aaa ctg cct gtt cca tgg 192
 Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 50 55 60

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cca | aca | cta | gtc | act | act | ctg | tgc | tat | ggg | gtt | caa | tgc | ttt | tca | aga | 240 |
| Pro | Thr | Leu | Val | Thr | Thr | Leu | Cys | Tyr | Gly | Val | Gln | Cys | Phe | Ser | Arg | |
| 65 | | | | | | 70 | | | | 75 | | | | | 80 | |
| tac | ccg | gat | cat | atg | aaa | cgg | cat | gac | ttt | ttc | aag | agt | gcc | atg | ccc | 288 |
| Tyr | Pro | Asp | His | Met | Lys | Arg | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro | |
| | | | | 85 | | | | | 90 | | | | | 95 | | |
| gaa | ggg | tat | gta | cag | gaa | agg | acc | atc | ttc | ttc | aaa | gat | gac | ggc | aac | 336 |
| Glu | Gly | Tyr | Val | Gln | Glu | Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| tac | aag | aca | cgt | gct | gaa | gtc | aag | ttt | gaa | ggg | gat | acc | ctt | gtt | aat | 384 |
| Tyr | Lys | Thr | Arg | Ala | Glu | Val | Lys | Phe | Glu | Gly | Asp | Thr | Leu | Val | Asn | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| aga | atc | gag | tta | aaa | ggg | att | gac | ttc | aag | gaa | gat | ggc | aac | att | ctg | 432 |
| Arg | Ile | Glu | Leu | Lys | Gly | Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| gga | cac | aaa | ttg | gaa | tac | aac | tat | aac | tca | cac | aat | gta | tac | atc | atg | 480 |
| Gly | His | Lys | Leu | Glu | Tyr | Asn | Tyr | Asn | Ser | His | Asn | Val | Tyr | Ile | Met | |
| 145 | | | | | 150 | | | | 155 | | | | | | 160 | |
| gca | gac | aaa | caa | aag | aat | gga | atc | aaa | gtg | aac | ttc | aag | acc | cgc | cac | 528 |
| Ala | Asp | Lys | Gln | Lys | Asn | Gly | Ile | Lys | Val | Asn | Phe | Lys | Thr | Arg | His | |
| | | | | 165 | | | | 170 | | | | | | 175 | | |
| aac | att | gaa | gat | gga | agc | gtt | caa | cta | gca | gac | cat | tat | caa | caa | aat | 576 |
| Asn | Ile | Glu | Asp | Gly | Ser | Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| act | cca | att | ggc | gat | ggc | cct | gtc | ctt | tta | cca | gac | aac | cat | tac | ctg | 624 |
| Thr | Pro | Ile | Gly | Asp | Gly | Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| tcc | aca | caa | tct | gcc | ctt | tcg | aaa | gat | ccc | aac | gaa | aag | aga | gac | cac | 672 |
| Ser | Thr | Gln | Ser | Ala | Leu | Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | |
| | 210 | | | | | 215 | | | | | 220 | | | | | |
| atg | gtc | ctt | ctt | gag | ttt | gta | aca | gct | gct | ggg | att | aca | cat | ggc | atg | 720 |
| Met | Val | Leu | Leu | Glu | Phe | Val | Thr | Ala | Ala | Gly | Ile | Thr | His | Gly | Met | |
| 225 | | | | | 230 | | | | 235 | | | | | | 240 | |
| gat | gaa | ctg | tac | aac | acc | ggg | atg | tct | aca | ggg | gtg | cct | tcg | ggg | tca | 768 |
| Asp | Glu | Leu | Tyr | Asn | Thr | Gly | Met | Ser | Thr | Gly | Val | Pro | Ser | Gly | Ser | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| agt | gct | gcc | act | ggc | agt | aat | cga | aga | ctc | cag | cag | aca | caa | aat | caa | 816 |
| Ser | Ala | Ala | Thr | Gly | Ser | Asn | Arg | Arg | Leu | Gln | Gln | Thr | Gln | Asn | Gln | |
| | | | 260 | | | | | 265 | | | | | 270 | | | |
| gta | gat | gag | gtg | gtt | gac | atc | atg | aga | gtc | aat | gtg | gat | aag | gtg | tta | 864 |
| Val | Asp | Glu | Val | Val | Asp | Ile | Met | Arg | Val | Asn | Val | Asp | Lys | Val | Leu | |
| | | 275 | | | | | 280 | | | | | 285 | | | | |
| gaa | aga | gac | cag | aag | ctc | tcg | gag | cta | gat | gac | cgc | gca | gat | gca | ctg | 912 |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|
| Glu | Arg | Asp | Gln | Lys | Leu | Ser | Glu | Leu | Asp | Asp | Arg | Ala | Asp | Ala | Leu | |
| 290 | | | | | | 295 | | | | | 300 | | | | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| cag | gca | ggt | gcc | tcg | cag | ttt | gaa | aca | agt | gct | gcc | aag | ttg | aag | aga | 960 |
| Gln | Ala | Gly | Ala | Ser | Gln | Phe | Glu | Thr | Ser | Ala | Ala | Lys | Leu | Lys | Arg | |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| aag | tat | tgg | tgg | aag | aac | tgc | aag | atg | tgg | gcg | ata | ggg | atc | agt | gtc | 1008 |
| Lys | Tyr | Trp | Trp | Lys | Asn | Cys | Lys | Met | Trp | Ala | Ile | Gly | Ile | Ser | Val | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|------|
| ctg | gtg | atc | att | gtc | atc | atc | atc | atc | gtg | tgg | tgt | gtc | tct | | | 1050 |
| Leu | Val | Ile | Ile | Val | Ile | Ile | Ile | Ile | Val | Trp | Cys | Val | Ser | | | |
| | | | | 340 | | | | | 345 | | | | 350 | | | |

taaatgagaa gaaaacgaca aaaggctagc aaaggagaag aactcttcac tggagttgtc 1110

ccaattcttg ttgaattaga tggatgatgtt aacggccaca agttctctgt cagtggagag 1170

ggtgaagggtg atgcaacata cggaaaactt accctgaagt tcatctgcac tactggcaaa 1230

ctgcctgttc catggccaac actagtcact actctgtgct atgggtgttca atgcttttca 1290

agatacccg atcatatgaa acggcatgac tttttcaaga gtgccatgcc cgaaggttat 1350

gtacaggaaa ggaccatctt cttcaaagat gacggcaact acaagacacg tgctgaagtc 1410

aagtttgaag gtgataccct tgttaataga atcgagttaa aaggatttga cttcaaggaa 1470

gatggcaaca ttctgggaca caaattggaa tacaactata actcacacaa tgtatacatc 1530

atggcagaca aacaaaagaa tggaatcaaa gtgaacttca agaccgcca caacattgaa 1590

gatggaagcg ttcaactagc agaccattat caacaaaata ctccaattgg cgatggccct 1650

gtccttttac cagacaacca ttacctgtcc acacaatctg ccctttcgaa agatcccaac 1710

gaaaagagag accacatggg ctttcttgag tttgtaacag ctgctgggat tacacatggc 1770

atggatgaac tgtacaacac cggatgtgtc acaggtgtgc cttcgggggc aagtgtgcc 1830

actggcagta atcgaagact ccagcagaca caaatcaag tagatgaggt ggttgacatc 1890

atgagagtca atgtggataa ggtgttagaa agagaccaga agctctcgga gctagatgac 1950

cgcgagatg cactgcaggc aggtgcctcg cagtttgaaa caagtgtgc caagttgaag 2010

agaaagtatt ggtggaagaa ctgcaagatg tgggcgatag ggatcagtg cctgggtgatc 2070

attgtcatca tcatcatcgt gtggtgtgtc tcttaa 2106

<210> 28
 <211> 350
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
NLS-Fred25-cellubrevin construct

<400> 28

Met Arg Arg Lys Arg Gln Lys Ala Ser Lys Gly Glu Glu Leu Phe Thr
1 5 10 15

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
20 25 30

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
35 40 45

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
50 55 60

Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg
65 70 75 80

Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro
85 90 95

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
100 105 110

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
115 120 125

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
130 135 140

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
145 150 155 160

Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His
165 170 175

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
180 185 190

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
195 200 205

Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
210 215 220

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met
225 230 235 240

Asp Glu Leu Tyr Asn Thr Gly Met Ser Thr Gly Val Pro Ser Gly Ser
245 250 255

Ser Ala Ala Thr Gly Ser Asn Arg Arg Leu Gln Gln Thr Gln Asn Gln
260 265 270

Val Asp Glu Val Val Asp Ile Met Arg Val Asn Val Asp Lys Val Leu

275 280 285
 Glu Arg Asp Gln Lys Leu Ser Glu Leu Asp Asp Arg Ala Asp Ala Leu
 290 295 300
 Gln Ala Gly Ala Ser Gln Phe Glu Thr Ser Ala Ala Lys Leu Lys Arg
 305 310 315 320
 Lys Tyr Trp Trp Lys Asn Cys Lys Met Trp Ala Ile Gly Ile Ser Val
 325 330 335
 Leu Val Ile Ile Val Ile Ile Ile Ile Val Trp Cys Val Ser
 340 345 350

<210> 29
 <211> 2088
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1041)

<220>
 <223> Description of Artificial Sequence:
 NLS-Fred25-synaptobrevin construct

<400> 29
 atg aga aga aaa cga caa aag gct agc aaa gga gaa gaa ctc ttc act 48
 Met Arg Arg Lys Arg Gln Lys Ala Ser Lys Gly Glu Glu Leu Phe Thr
 1 5 10 15
 gga gtt gtc cca att ctt gtt gaa tta gat ggt gat gtt aac ggc cac 96
 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 20 25 30
 aag ttc tct gtc agt gga gag ggt gaa ggt gat gca aca tac gga aaa 144
 Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
 35 40 45
 ctt acc ctg aag ttc atc tgc act act ggc aaa ctg cct gtt cca tgg 192
 Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
 50 55 60
 cca aca cta gtc act act ctg tgc tat ggt gtt caa tgc ttt tca aga 240
 Pro Thr Leu Val Thr Thr Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg
 65 70 75 80
 tac ccg gat cat atg aaa cgg cat gac ttt ttc aag agt gcc atg ccc 288
 Tyr Pro Asp His Met Lys Arg His Asp Phe Phe Lys Ser Ala Met Pro
 85 90 95
 gaa ggt tat gta cag gaa agg acc atc ttc ttc aaa gat gac ggc aac 336
 Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
 100 105 110

tac aag aca cgt gct gaa gtc aag ttt gaa ggt gat acc ctt gtt aat 384
 Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
 115 120 125

aga atc gag tta aaa ggt att gac ttc aag gaa gat ggc aac att ctg 432
 Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
 130 135 140

gga cac aaa ttg gaa tac aac tat aac tca cac aat gta tac atc atg 480
 Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
 145 150 155 160

gca gac aaa caa aag aat gga atc aaa gtg aac ttc aag acc cgc cac 528
 Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Thr Arg His
 165 170 175

aac att gaa gat gga agc gtt caa cta gca gac cat tat caa caa aat 576
 Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
 180 185 190

act cca att ggc gat ggc cct gtc ctt tta cca gac aac cat tac ctg 624
 Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
 195 200 205

tcc aca caa tct gcc ctt tcg aaa gat ccc aac gaa aag aga gac cac 672
 Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
 210 215 220

atg gtc ctt ctt gag ttt gta aca gct gct ggg att aca cat ggc atg 720
 Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr His Gly Met
 225 230 235 240

gat gaa ctg tac aac acc ggt atg tct aca ggt cca act gct gcc act 768
 Asp Glu Leu Tyr Asn Thr Gly Met Ser Thr Gly Pro Thr Ala Ala Thr
 245 250 255

ggc agt aat cga aga ctt cag cag aca caa aat caa gta gat gag gtg 816
 Gly Ser Asn Arg Arg Leu Gln Gln Thr Gln Asn Gln Val Asp Glu Val
 260 265 270

gtg gac ata atg cga gtt aac gtg gac aag gtt ctg gaa aga gac cag 864
 Val Asp Ile Met Arg Val Asn Val Asp Lys Val Leu Glu Arg Asp Gln
 275 280 285

aag ctc tct gag tta gac gac cgt gca gac gca ctg cag gca ggc gct 912
 Lys Leu Ser Glu Leu Asp Asp Arg Ala Asp Ala Leu Gln Ala Gly Ala
 290 295 300

tct caa ttt gaa acg agc gca gcc aag ttg aag agg aaa tat tgg tgg 960
 Ser Gln Phe Glu Thr Ser Ala Ala Lys Leu Lys Arg Lys Tyr Trp Trp
 305 310 315 320

aag aat tgc aag atg tgg gca atc ggg att act gtt ctg gtt atc ttc 1008
 Lys Asn Cys Lys Met Trp Ala Ile Gly Ile Thr Val Leu Val Ile Phe
 325 330 335

atc atc atc atc atc gtg tgg gtt gtc tct tca tgaatgagaa gaaaacgaca 1061

Ile Ile Ile Ile Ile Val Trp Val Val Ser Ser
 340 345

aaaggctagc aaaggagaag aactcttcac tggagttgtc ccaattcttg ttgaattaga 1121
 tggatgatgtt aacggccaca agttctctgt cagtggagag ggtgaagggtg atgcaacata 1181
 cggaaaactt accctgaagt tcatctgcac tactggcaaa ctgcctgttc catggccaac 1241
 actagtcact actctgtgct atgggtgttca atgcttttca agatacccg atcatatgaa 1301
 acggcatgac tttttcaaga gtgccatgcc cgaaggttat gtacaggaaa ggaccatctt 1361
 cttcaaagat gacggcaact acaagacacg tgctgaagtc aagtttgaag gtgataccct 1421
 tgттаataga atcgagttaa aaggatttga cttcaaggaa gatggcaaca ttctgggaca 1481
 caaattggaa tacaactata actcacacaa tgtatacatc atggcagaca aacaaaagaa 1541
 tggaatcaaa gtgaacttca agaccgcga caacattgaa gatggaagcg ttcaactagc 1601
 agaccattat caacaaaata ctccaattgg cgatggccct gtccttttac cagacaacca 1661
 ttacctgtcc acacaatctg ccttttcgaa agatcccaac gaaaagagag accacatggt 1721
 ccttcttgag tttgtaacag ctgctgggat tacacatggc atggatgaac tgtacaacac 1781
 cggtatgtct acaggtccaa ctgctgccac tggcagtaat cgaagacttc agcagacaca 1841
 aaatcaagta gatgaggtgg tggacataat gcgagttaac gtggacaagg ttctggaaaag 1901
 agaccagaag ctctctgagt tagacgaccg tgcagacgca ctgcaggcag gcgcttctca 1961
 atttgaaacg agcgagcca agttgaagag gaaatattgg tggaagaatt gcaagatgtg 2021
 ggcaatcggg attactgttc tggttatctt catcatcatc atcatcgtgt gggttgtctc 2081
 ttcatga 2088

<210> 30
 <211> 347
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 NLS-Fred25-synaptobrevin construct

b1
 <400> 30
 Met Arg Arg Lys Arg Gln Lys Ala Ser Lys Gly Glu Glu Leu Phe Thr
 1 5 10 15
 Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
 20 25 30
 Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys

| 35 | | | | | 40 | | | | | 45 | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Thr | Leu | Lys | Phe | Ile | Cys | Thr | Thr | Gly | Lys | Leu | Pro | Val | Pro | Trp |
| 50 | | | | | | 55 | | | | | 60 | | | | |
| Pro | Thr | Leu | Val | Thr | Thr | Leu | Cys | Tyr | Gly | Val | Gln | Cys | Phe | Ser | Arg |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Tyr | Pro | Asp | His | Met | Lys | Arg | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Glu | Gly | Tyr | Val | Gln | Glu | Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Tyr | Lys | Thr | Arg | Ala | Glu | Val | Lys | Phe | Glu | Gly | Asp | Thr | Leu | Val | Asn |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Arg | Ile | Glu | Leu | Lys | Gly | Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Gly | His | Lys | Leu | Glu | Tyr | Asn | Tyr | Asn | Ser | His | Asn | Val | Tyr | Ile | Met |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Ala | Asp | Lys | Gln | Lys | Asn | Gly | Ile | Lys | Val | Asn | Phe | Lys | Thr | Arg | His |
| | | | | 165 | | | | | 170 | | | | | 175 | |
| Asn | Ile | Glu | Asp | Gly | Ser | Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn |
| | | 180 | | | | | | 185 | | | | | 190 | | |
| Thr | Pro | Ile | Gly | Asp | Gly | Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu |
| | | 195 | | | | | 200 | | | | | 205 | | | |
| Ser | Thr | Gln | Ser | Ala | Leu | Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His |
| | 210 | | | | | 215 | | | | | 220 | | | | |
| Met | Val | Leu | Leu | Glu | Phe | Val | Thr | Ala | Ala | Gly | Ile | Thr | His | Gly | Met |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 |
| Asp | Glu | Leu | Tyr | Asn | Thr | Gly | Met | Ser | Thr | Gly | Pro | Thr | Ala | Ala | Thr |
| | | | | 245 | | | | | 250 | | | | | 255 | |
| Gly | Ser | Asn | Arg | Arg | Leu | Gln | Gln | Thr | Gln | Asn | Gln | Val | Asp | Glu | Val |
| | | | 260 | | | | | 265 | | | | | 270 | | |
| Val | Asp | Ile | Met | Arg | Val | Asn | Val | Asp | Lys | Val | Leu | Glu | Arg | Asp | Gln |
| | | 275 | | | | | 280 | | | | | 285 | | | |
| Lys | Leu | Ser | Glu | Leu | Asp | Asp | Arg | Ala | Asp | Ala | Leu | Gln | Ala | Gly | Ala |
| | 290 | | | | | 295 | | | | | 300 | | | | |
| Ser | Gln | Phe | Glu | Thr | Ser | Ala | Ala | Lys | Leu | Lys | Arg | Lys | Tyr | Trp | Trp |
| 305 | | | | | 310 | | | | | 315 | | | | | 320 |
| Lys | Asn | Cys | Lys | Met | Trp | Ala | Ile | Gly | Ile | Thr | Val | Leu | Val | Ile | Phe |
| | | | | 325 | | | | | 330 | | | | | 335 | |
| Ile | Ile | Ile | Ile | Ile | Val | Trp | Val | Val | Ser | Ser | | | | | |

340

345

<210> 31
 <211> 3171
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(3168)

<220>
 <223> Description of Artificial Sequence:
 NLS-EYFP-MAPKDM-EBFP construct

<400> 31
 atg agg ccc aga aga aag gtg agc aag ggc gag gag ctg ttc acc ggg 48
 Met Arg Pro Arg Arg Lys Val Ser Lys Gly Glu Glu Leu Phe Thr Gly
 1 5 10 15

gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc cac aag 96
 Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys
 20 25 30

ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg 144
 Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu
 35 40 45

acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc 192
 Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro
 50 55 60

acc ctc gtg acc acc ttc ggc tac ggc ctg cag tgc ttc gcc cgc tac 240
 Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr
 65 70 75 80

ccc gac cac atg aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa 288
 Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu
 85 90 95

ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac ggc aac tac 336
 Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr
 100 105 110

aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc 384
 Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg
 115 120 125

atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg 432
 Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly
 130 135 140

cac aag ctg gag tac aac tac aac agc cac aac gtc tat atc atg gcc 480
 His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala
 145 150 155 160

| | |
|--|------|
| gac aag cag aag aac ggc atc aag gtg aac ttc aag atc cgc cac aac | 528 |
| Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn | |
| 165 170 175 | |
| atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc | 576 |
| Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr | |
| 180 185 190 | |
| ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc | 624 |
| Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser | |
| 195 200 205 | |
| tac cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg | 672 |
| Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met | |
| 210 215 220 | |
| gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac | 720 |
| Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp | |
| 225 230 235 240 | |
| gag ctg tac aag aag gga gac gaa gtg gac gga gcc gac ctc agt ctt | 768 |
| Glu Leu Tyr Lys Lys Gly Asp Glu Val Asp Gly Ala Asp Leu Ser Leu | |
| 245 250 255 | |
| gtg gat gcg ttg aca gaa cca cct cca gaa att gag gga gaa ata aag | 816 |
| Val Asp Ala Leu Thr Glu Pro Pro Pro Glu Ile Glu Gly Glu Ile Lys | |
| 260 265 270 | |
| cga gac ttc atg gct gcg ctg gag gca gag ccc tat gat gac atc gtg | 864 |
| Arg Asp Phe Met Ala Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val | |
| 275 280 285 | |
| gga gaa act gtg gag aaa act gag ttt att cct ctc ctg gat ggt gat | 912 |
| Gly Glu Thr Val Glu Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp | |
| 290 295 300 | |
| gag aaa acc ggg aac tca gag tcc aaa aag aaa ccc tgc tta gac act | 960 |
| Glu Lys Thr Gly Asn Ser Glu Ser Lys Lys Lys Pro Cys Leu Asp Thr | |
| 305 310 315 320 | |
| agc cag gtt gaa ggt atc cca tct tct aaa cca aca ctc cta gcc aat | 1008 |
| Ser Gln Val Glu Gly Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn | |
| 325 330 335 | |
| ggt gat cat gga atg gag ggg aat aac act gca ggg tct cca act gac | 1056 |
| Gly Asp His Gly Met Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp | |
| 340 345 350 | |
| ttc ctt gaa gag aga gtg gac tat ccg gat tat cag agc agc cag aac | 1104 |
| Phe Leu Glu Glu Arg Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn | |
| 355 360 365 | |
| tggt cca gaa gat gca agc ttt tgt ttc cag cct cag caa gtg tta gat | 1152 |
| Trp Pro Glu Asp Ala Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp | |
| 370 375 380 | |
| act gac cag gct gag ccc ttt aac gag cac cgt gat gat ggt ttg gca | 1200 |

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Thr | Asp | Gln | Ala | Glu | Pro | Phe | Asn | Glu | His | Arg | Asp | Asp | Gly | Leu | Ala | | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | | |
| gat | ctg | ctc | ttt | gtc | tcc | agt | gga | ccc | acg | aac | gct | tct | gca | ttt | aca | 1248 | |
| Asp | Leu | Leu | Phe | Val | Ser | Ser | Gly | Pro | Thr | Asn | Ala | Ser | Ala | Phe | Thr | | |
| | | | | 405 | | | | | 410 | | | | | 415 | | | |
| gag | cga | gac | aat | cct | tca | gaa | gac | agt | tac | ggg | atg | ctt | ccc | tgt | gac | 1296 | |
| Glu | Arg | Asp | Asn | Pro | Ser | Glu | Asp | Ser | Tyr | Gly | Met | Leu | Pro | Cys | Asp | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | |
| tca | ttt | gct | tcc | acg | gct | gtt | gta | tct | cag | gag | tgg | tct | gtg | gga | gcc | 1344 | |
| Ser | Phe | Ala | Ser | Thr | Ala | Val | Val | Ser | Gln | Glu | Trp | Ser | Val | Gly | Ala | | |
| | | 435 | | | | | 440 | | | | | 445 | | | | | |
| cca | aac | tct | cca | tgt | tca | gag | tcc | tgt | gtc | tcc | cca | gag | gtt | act | ata | 1392 | |
| Pro | Asn | Ser | Pro | Cys | Ser | Glu | Ser | Cys | Val | Ser | Pro | Glu | Val | Thr | Ile | | |
| | 450 | | | | | 455 | | | | | 460 | | | | | | |
| gaa | acc | cta | cag | cca | gca | aca | gag | ctc | tcc | aag | gca | gca | gaa | gtg | gaa | 1440 | |
| Glu | Thr | Leu | Gln | Pro | Ala | Thr | Glu | Leu | Ser | Lys | Ala | Ala | Glu | Val | Glu | | |
| 465 | | | | | 470 | | | | 475 | | | | | | 480 | | |
| tca | gtg | aaa | gag | cag | ctg | cca | gct | aaa | gca | ttg | gaa | acg | atg | gca | gag | 1488 | |
| Ser | Val | Lys | Glu | Gln | Leu | Pro | Ala | Lys | Ala | Leu | Glu | Thr | Met | Ala | Glu | | |
| | | | | 485 | | | | 490 | | | | | | 495 | | | |
| cag | acc | act | gat | gtg | gtg | cac | tct | cca | tcc | aca | gac | aca | aca | cca | ggc | 1536 | |
| Gln | Thr | Thr | Asp | Val | Val | His | Ser | Pro | Ser | Thr | Asp | Thr | Thr | Pro | Gly | | |
| | | | 500 | | | | | 505 | | | | | 510 | | | | |
| cca | gac | aca | gag | gca | gca | ctg | gct | aaa | gac | ata | gaa | gag | atc | acc | aag | 1584 | |
| Pro | Asp | Thr | Glu | Ala | Ala | Leu | Ala | Lys | Asp | Ile | Glu | Glu | Ile | Thr | Lys | | |
| | | 515 | | | | | 520 | | | | | 525 | | | | | |
| cca | gat | gtg | ata | ttg | gca | aat | gtc | acg | cag | cca | tct | act | gaa | tcg | gat | 1632 | |
| Pro | Asp | Val | Ile | Leu | Ala | Asn | Val | Thr | Gln | Pro | Ser | Thr | Glu | Ser | Asp | | |
| | | 530 | | | | 535 | | | | | 540 | | | | | | |
| atg | ttc | ctg | gcc | cag | gac | atg | gaa | cta | ctc | aca | gga | aca | gag | gca | gcc | 1680 | |
| Met | Phe | Leu | Ala | Gln | Asp | Met | Glu | Leu | Leu | Thr | Gly | Thr | Glu | Ala | Ala | | |
| 545 | | | | | 550 | | | | | 555 | | | | | 560 | | |
| cac | gct | aac | aat | atc | ata | ttg | cct | aca | gaa | cca | gac | gaa | tct | tca | acc | 1728 | |
| His | Ala | Asn | Asn | Ile | Ile | Leu | Pro | Thr | Glu | Pro | Asp | Glu | Ser | Ser | Thr | | |
| | | | | 565 | | | | 570 | | | | | | 575 | | | |
| aag | gat | gta | gca | cca | cct | atg | gaa | gaa | gaa | att | gtc | cca | ggc | aat | gat | 1776 | |
| Lys | Asp | Val | Ala | Pro | Pro | Met | Glu | Glu | Glu | Ile | Val | Pro | Gly | Asn | Asp | | |
| | | | 580 | | | | | 585 | | | | | 590 | | | | |
| acg | aca | tcc | ccc | aaa | gaa | aca | gag | aca | aca | ctt | cca | ata | aaa | atg | gac | 1824 | |
| Thr | Thr | Ser | Pro | Lys | Glu | Thr | Glu | Thr | Thr | Leu | Pro | Ile | Lys | Met | Asp | | |
| | | 595 | | | | | 600 | | | | | 605 | | | | | |
| ttg | gca | cca | cct | gag | gat | gtg | tta | ctt | acc | aaa | gaa | aca | gaa | cta | gcc | 1872 | |
| Leu | Ala | Pro | Pro | Glu | Asp | Val | Leu | Leu | Thr | Lys | Glu | Thr | Glu | Leu | Ala | | |

| 610 | 615 | 620 | |
|---|-----|-----|------|
| cca gcc aag ggc atg gtt tca ctc tca gaa ata gaa gag gct ctg gca Pro Ala Lys Gly Met Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala 625 630 635 640 | | | 1920 |
| aag aat gat gtt cgc tct gca gaa ata cct gtg gct cag gag aca gtg Lys Asn Asp Val Arg Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val 645 650 655 | | | 1968 |
| gtc tca gaa aca gag gtg gtc ctg gca aca gaa gtg gta ctg ccc tca Val Ser Glu Thr Glu Val Val Leu Ala Thr Glu Val Val Leu Pro Ser 660 665 670 | | | 2016 |
| gat ccc ata aca aca ttg aca aag gat gtg aca ctc ccc tta gaa gca Asp Pro Ile Thr Thr Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala 675 680 685 | | | 2064 |
| gag aga ccg ttg gtg acg gac atg act cca tct ctg gaa aca gaa atg Glu Arg Pro Leu Val Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met 690 695 700 | | | 2112 |
| acc cta ggc aaa gag aca gct cca ccc aca gaa aca aat ttg ggc atg Thr Leu Gly Lys Glu Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met 705 710 715 720 | | | 2160 |
| gcc aaa gac atg tct cca ctc cca gaa tca gaa gtg act ctg ggc aag Ala Lys Asp Met Ser Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys 725 730 735 | | | 2208 |
| gac gtg gtt ata ctt cca gaa aca aag gtg gct gag ttt aac aat gtg Asp Val Val Ile Leu Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val 740 745 750 | | | 2256 |
| act cca ctt tca gaa gaa gag gta acc tca gtc aag gac atg tct ccg Thr Pro Leu Ser Glu Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro 755 760 765 | | | 2304 |
| tct gca gaa aca gag gct ccc ctg gct aag aat gct gat ctg cac tca Ser Ala Glu Thr Glu Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser 770 775 780 | | | 2352 |
| gga aca gag ctg att gtg gac aac agc atg gct cca gcc tcc gat ctt Gly Thr Glu Leu Ile Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu 785 790 795 800 | | | 2400 |
| gca ctg ccc ttg gaa aca aaa gta gca aca gtt cca att aaa gac aaa Ala Leu Pro Leu Glu Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys 805 810 815 | | | 2448 |
| gga atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc Gly Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile 820 825 830 | | | 2496 |
| ctg gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser 835 840 845 | | | 2544 |

ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc 2592
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 850 855 860

 atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc 2640
 Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 865 870 875 880

 acc ctg acc cac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg 2688
 Thr Leu Thr His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 885 890 895

 aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag 2736
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 900 905 910

 gag cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc 2784
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 915 920 925

 gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag 2832
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 930 935 940

 ggc atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag 2880
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 945 950 955 960

 tac aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag 2928
 Tyr Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 965 970 975

 aac ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc 2976
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 980 985 990

 agc gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac 3024
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 995 1000 1005

 ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc 3072
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 1010 1015 1020

 ctg agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag 3120
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 1025 1030 1035 1040

 ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag 3168
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 1045 1050 1055

 tag 3171

<210> 32

<211> 1056
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
 NLS-EYFP-MAPKDM-EBFP construct

<400> 32

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Arg | Pro | Arg | Arg | Lys | Val | Ser | Lys | Gly | Glu | Glu | Leu | Phe | Thr | Gly | 1 | 5 | 10 | 15 |
| Val | Val | Pro | Ile | Leu | Val | Glu | Leu | Asp | Gly | Asp | Val | Asn | Gly | His | Lys | 20 | 25 | 30 | |
| Phe | Ser | Val | Ser | Gly | Glu | Gly | Glu | Gly | Asp | Ala | Thr | Tyr | Gly | Lys | Leu | 35 | 40 | 45 | |
| Thr | Leu | Lys | Phe | Ile | Cys | Thr | Thr | Gly | Lys | Leu | Pro | Val | Pro | Trp | Pro | 50 | 55 | 60 | |
| Thr | Leu | Val | Thr | Thr | Phe | Gly | Tyr | Gly | Leu | Gln | Cys | Phe | Ala | Arg | Tyr | 65 | 70 | 75 | 80 |
| Pro | Asp | His | Met | Lys | Gln | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro | Glu | 85 | 90 | 95 | |
| Gly | Tyr | Val | Gln | Glu | Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn | Tyr | 100 | 105 | 110 | |
| Lys | Thr | Arg | Ala | Glu | Val | Lys | Phe | Glu | Gly | Asp | Thr | Leu | Val | Asn | Arg | 115 | 120 | 125 | |
| Ile | Glu | Leu | Lys | Gly | Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu | Gly | 130 | 135 | 140 | |
| His | Lys | Leu | Glu | Tyr | Asn | Tyr | Asn | Ser | His | Asn | Val | Tyr | Ile | Met | Ala | 145 | 150 | 155 | 160 |
| Asp | Lys | Gln | Lys | Asn | Gly | Ile | Lys | Val | Asn | Phe | Lys | Ile | Arg | His | Asn | 165 | 170 | 175 | |
| Ile | Glu | Asp | Gly | Ser | Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn | Thr | 180 | 185 | 190 | |
| Pro | Ile | Gly | Asp | Gly | Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | 195 | 200 | 205 | |
| Tyr | Gln | Ser | Ala | Leu | Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | 210 | 215 | 220 | |
| Val | Leu | Leu | Glu | Phe | Val | Thr | Ala | Ala | Gly | Ile | Thr | Leu | Gly | Met | Asp | 225 | 230 | 235 | 240 |
| Glu | Leu | Tyr | Lys | Lys | Gly | Asp | Glu | Val | Asp | Gly | Ala | Asp | Leu | Ser | Leu | 245 | 250 | 255 | |

Val Asp Ala Leu Thr Glu Pro Pro Pro Glu Ile Glu Gly Glu Ile Lys
 260 265 270
 Arg Asp Phe Met Ala Ala Leu Glu Ala Glu Pro Tyr Asp Asp Ile Val
 275 280 285
 Gly Glu Thr Val Glu Lys Thr Glu Phe Ile Pro Leu Leu Asp Gly Asp
 290 295 300
 Glu Lys Thr Gly Asn Ser Glu Ser Lys Lys Lys Pro Cys Leu Asp Thr
 305 310 315 320
 Ser Gln Val Glu Gly Ile Pro Ser Ser Lys Pro Thr Leu Leu Ala Asn
 325 330 335
 Gly Asp His Gly Met Glu Gly Asn Asn Thr Ala Gly Ser Pro Thr Asp
 340 345 350
 Phe Leu Glu Glu Arg Val Asp Tyr Pro Asp Tyr Gln Ser Ser Gln Asn
 355 360 365
 Trp Pro Glu Asp Ala Ser Phe Cys Phe Gln Pro Gln Gln Val Leu Asp
 370 375 380
 Thr Asp Gln Ala Glu Pro Phe Asn Glu His Arg Asp Asp Gly Leu Ala
 385 390 395 400
 Asp Leu Leu Phe Val Ser Ser Gly Pro Thr Asn Ala Ser Ala Phe Thr
 405 410 415
 Glu Arg Asp Asn Pro Ser Glu Asp Ser Tyr Gly Met Leu Pro Cys Asp
 420 425 430
 Ser Phe Ala Ser Thr Ala Val Val Ser Gln Glu Trp Ser Val Gly Ala
 435 440 445
 Pro Asn Ser Pro Cys Ser Glu Ser Cys Val Ser Pro Glu Val Thr Ile
 450 455 460
 Glu Thr Leu Gln Pro Ala Thr Glu Leu Ser Lys Ala Ala Glu Val Glu
 465 470 475 480
 Ser Val Lys Glu Gln Leu Pro Ala Lys Ala Leu Glu Thr Met Ala Glu
 485 490 495
 Gln Thr Thr Asp Val Val His Ser Pro Ser Thr Asp Thr Thr Pro Gly
 500 505 510
 Pro Asp Thr Glu Ala Ala Leu Ala Lys Asp Ile Glu Glu Ile Thr Lys
 515 520 525
 Pro Asp Val Ile Leu Ala Asn Val Thr Gln Pro Ser Thr Glu Ser Asp
 530 535 540
 Met Phe Leu Ala Gln Asp Met Glu Leu Leu Thr Gly Thr Glu Ala Ala
 545 550 555 560

His Ala Asn Asn Ile Ile Leu Pro Thr Glu Pro Asp Glu Ser Ser Thr
 565 570 575
 Lys Asp Val Ala Pro Pro Met Glu Glu Glu Ile Val Pro Gly Asn Asp
 580 585 590
 Thr Thr Ser Pro Lys Glu Thr Glu Thr Thr Leu Pro Ile Lys Met Asp
 595 600 605
 Leu Ala Pro Pro Glu Asp Val Leu Leu Thr Lys Glu Thr Glu Leu Ala
 610 615 620
 Pro Ala Lys Gly Met Val Ser Leu Ser Glu Ile Glu Glu Ala Leu Ala
 625 630 635 640
 Lys Asn Asp Val Arg Ser Ala Glu Ile Pro Val Ala Gln Glu Thr Val
 645 650 655
 Val Ser Glu Thr Glu Val Val Leu Ala Thr Glu Val Val Leu Pro Ser
 660 665 670
 Asp Pro Ile Thr Thr Leu Thr Lys Asp Val Thr Leu Pro Leu Glu Ala
 675 680 685
 Glu Arg Pro Leu Val Thr Asp Met Thr Pro Ser Leu Glu Thr Glu Met
 690 695 700
 Thr Leu Gly Lys Glu Thr Ala Pro Pro Thr Glu Thr Asn Leu Gly Met
 705 710 715 720
 Ala Lys Asp Met Ser Pro Leu Pro Glu Ser Glu Val Thr Leu Gly Lys
 725 730 735
 Asp Val Val Ile Leu Pro Glu Thr Lys Val Ala Glu Phe Asn Asn Val
 740 745 750
 Thr Pro Leu Ser Glu Glu Glu Val Thr Ser Val Lys Asp Met Ser Pro
 755 760 765
 Ser Ala Glu Thr Glu Ala Pro Leu Ala Lys Asn Ala Asp Leu His Ser
 770 775 780
 Gly Thr Glu Leu Ile Val Asp Asn Ser Met Ala Pro Ala Ser Asp Leu
 785 790 795 800
 Ala Leu Pro Leu Glu Thr Lys Val Ala Thr Val Pro Ile Lys Asp Lys
 805 810 815
 Gly Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
 820 825 830
 Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
 835 840 845
 Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
 850 855 860

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
 865 870 875 880
 Thr Leu Thr His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met
 885 890 895
 Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
 900 905 910
 Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
 915 920 925
 Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
 930 935 940
 Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
 945 950 955 960
 Tyr Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
 965 970 975
 Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
 980 985 990
 Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
 995 1000 1005
 Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala
 1010 1015 1020
 Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
 1025 1030 1035 1040
 Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 1045 1050 1055

<210> 33
 <211> 1623
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(1623)

<220>
 <223> Description of Artificial Sequence:
 YFP-NLS-CP3-multiple DEVD-CFP-Annexin II construct

<400> 33
 atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly

| 20 | | | | | | | | | | 25 | | | | | | | | | | 30 | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|----|--|--|--|--|--|--|--|--|--|--|
| gag | ggc | gag | ggc | gat | gcc | acc | tac | ggc | aag | ctg | acc | ctg | aag | ttc | atc | 144 | | | | | | | | | | | | | | |
| Glu | Gly | Glu | Gly | Asp | Ala | Thr | Tyr | Gly | Lys | Leu | Thr | Leu | Lys | Phe | Ile | | | | | | | | | | | | | | | |
| 35 | | | | 40 | | | | 45 | | | | | | | | | | | | | | | | | | | | | | |
| tgc | acc | acc | ggc | aag | ctg | ccc | gtg | ccc | tgg | ccc | acc | ctc | gtg | acc | acc | 192 | | | | | | | | | | | | | | |
| Cys | Thr | Thr | Gly | Lys | Leu | Pro | Val | Pro | Trp | Pro | Thr | Leu | Val | Thr | Thr | | | | | | | | | | | | | | | |
| 50 | | | 55 | | | 60 | | | | | | | | | | | | | | | | | | | | | | | | |
| ttc | ggc | tac | ggc | ctg | cag | tgc | ttc | gcc | cgc | tac | ccc | gac | cac | atg | aag | 240 | | | | | | | | | | | | | | |
| Phe | Gly | Tyr | Gly | Leu | Gln | Cys | Phe | Ala | Arg | Tyr | Pro | Asp | His | Met | Lys | | | | | | | | | | | | | | | |
| 65 | | | | 70 | | | | 75 | | | | | | 80 | | | | | | | | | | | | | | | | |
| cag | cac | gac | ttc | ttc | aag | tcc | gcc | atg | ccc | gaa | ggc | tac | gtc | cag | gag | 288 | | | | | | | | | | | | | | |
| Gln | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro | Glu | Gly | Tyr | Val | Gln | Glu | | | | | | | | | | | | | | | |
| 85 | | | | 90 | | | | 95 | | | | | | | | | | | | | | | | | | | | | | |
| cgc | acc | atc | ttc | ttc | aag | gac | gac | ggc | aac | tac | aag | acc | cgc | gcc | gag | 336 | | | | | | | | | | | | | | |
| Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn | Tyr | Lys | Thr | Arg | Ala | Glu | | | | | | | | | | | | | | | |
| 100 | | | | | | 105 | | | | | | 110 | | | | | | | | | | | | | | | | | | |
| gtg | aag | ttc | gag | ggc | gac | acc | ctg | gtg | aac | cgc | atc | gag | ctg | aag | ggc | 384 | | | | | | | | | | | | | | |
| Val | Lys | Phe | Glu | Gly | Asp | Thr | Leu | Val | Asn | Arg | Ile | Glu | Leu | Lys | Gly | | | | | | | | | | | | | | | |
| 115 | | | | | | 120 | | | | | | 125 | | | | | | | | | | | | | | | | | | |
| atc | gac | ttc | aag | gag | gac | ggc | aac | atc | ctg | ggg | cac | aag | ctg | gag | tac | 432 | | | | | | | | | | | | | | |
| Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu | Gly | His | Lys | Leu | Glu | Tyr | | | | | | | | | | | | | | | |
| 130 | | | | | | 135 | | | | | | 140 | | | | | | | | | | | | | | | | | | |
| aac | tac | aac | agc | cac | aac | gtc | tat | atc | atg | gcc | gac | aag | cag | aag | aac | 480 | | | | | | | | | | | | | | |
| Asn | Tyr | Asn | Ser | His | Asn | Val | Tyr | Ile | Met | Ala | Asp | Lys | Gln | Lys | Asn | | | | | | | | | | | | | | | |
| 145 | | | | 150 | | | | 155 | | | | 160 | | | | | | | | | | | | | | | | | | |
| ggc | atc | aag | gtg | aac | ttc | aag | atc | cgc | cac | aac | atc | gag | gac | ggc | agc | 528 | | | | | | | | | | | | | | |
| Gly | Ile | Lys | Val | Asn | Phe | Lys | Ile | Arg | His | Asn | Ile | Glu | Asp | Gly | Ser | | | | | | | | | | | | | | | |
| 165 | | | | 170 | | | | 175 | | | | | | | | | | | | | | | | | | | | | | |
| gtg | cag | ctc | gcc | gac | cac | tac | cag | cag | aac | acc | ccc | atc | ggc | gac | ggc | 576 | | | | | | | | | | | | | | |
| Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn | Thr | Pro | Ile | Gly | Asp | Gly | | | | | | | | | | | | | | | |
| 180 | | | | | | 185 | | | | | | 190 | | | | | | | | | | | | | | | | | | |
| ccc | gtg | ctg | ctg | ccc | gac | aac | cac | tac | ctg | agc | tac | cag | tcc | gcc | ctg | 624 | | | | | | | | | | | | | | |
| Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | Tyr | Gln | Ser | Ala | Leu | | | | | | | | | | | | | | | |
| 195 | | | | | | 200 | | | | | | 205 | | | | | | | | | | | | | | | | | | |
| agc | aaa | gac | ccc | aac | gag | aag | cgc | gat | cac | atg | gtc | ctg | ctg | gag | ttc | 672 | | | | | | | | | | | | | | |
| Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu | Leu | Glu | Phe | | | | | | | | | | | | | | | |
| 210 | | | | 215 | | | | 220 | | | | | | | | | | | | | | | | | | | | | | |
| gtg | acc | gcc | gcc | ggg | atc | act | ctc | ggc | atg | gac | gag | ctg | tac | aag | tcc | 720 | | | | | | | | | | | | | | |
| Val | Thr | Ala | Ala | Gly | Ile | Thr | Leu | Gly | Met | Asp | Glu | Leu | Tyr | Lys | Ser | | | | | | | | | | | | | | | |
| 225 | | | | 230 | | | | 235 | | 240 | | | | | | | | | | | | | | | | | | | | |
| gga | aga | agg | aaa | cga | caa | aag | cga | tcg | gca | ggg | gac | gaa | gtt | gat | gca | 768 | | | | | | | | | | | | | | |
| Gly | Arg | Arg | Lys | Arg | Gln | Lys | Arg | Ser | Ala | Gly | Asp | Glu | Val | Asp | Ala | | | | | | | | | | | | | | | |
| 245 | | | | | | 250 | | | | | | 255 | | | | | | | | | | | | | | | | | | |

| | |
|---|------|
| ggt gac gaa gtt gat gca ggt gac gaa gtt gat gca ggt gac gaa gtt | 816 |
| Gly Asp Glu Val Asp Ala Gly Asp Glu Val Asp Ala Gly Asp Glu Val | |
| 260 265 270 | |
| gac gca ggt agt act atg gtg agc aag ggc gag gag ctg ttc acc ggg | 864 |
| Asp Ala Gly Ser Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly | |
| 275 280 285 | |
| gtg gtg ccc atc ctg gtc gag ctg gac ggc gac gta aac ggc cac aag | 912 |
| Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys | |
| 290 295 300 | |
| ttc agc gtg tcc ggc gag ggc gag ggc gat gcc acc tac ggc aag ctg | 960 |
| Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu | |
| 305 310 315 320 | |
| acc ctg aag ttc atc tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc | 1008 |
| Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro | |
| 325 330 335 | |
| acc ctc gtg acc acc ctg acc tgg ggc gtg cag tgc ttc agc cgc tac | 1056 |
| Thr Leu Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr | |
| 340 345 350 | |
| ccc gac cac atg aag cag cac gac ttc ttc aag tcc gcc atg ccc gaa | 1104 |
| Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu | |
| 355 360 365 | |
| ggc tac gtc cag gag cgc acc atc ttc ttc aag gac gac ggc aac tac | 1152 |
| Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr | |
| 370 375 380 | |
| aag acc cgc gcc gag gtg aag ttc gag ggc gac acc ctg gtg aac cgc | 1200 |
| Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg | |
| 385 390 395 400 | |
| atc gag ctg aag ggc atc gac ttc aag gag gac ggc aac atc ctg ggg | 1248 |
| Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly | |
| 405 410 415 | |
| cac aag ctg gag tac aac tac atc agc cac aac gtc tat atc acc gcc | 1296 |
| His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala | |
| 420 425 430 | |
| gac aag cag aag aac ggc atc aag gcc aac ttc aag atc cgc cac aac | 1344 |
| Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn | |
| 435 440 445 | |
| atc gag gac ggc agc gtg cag ctc gcc gac cac tac cag cag aac acc | 1392 |
| Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr | |
| 450 455 460 | |
| ccc atc ggc gac ggc ccc gtg ctg ctg ccc gac aac cac tac ctg agc | 1440 |
| Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser | |
| 465 470 475 480 | |

| | |
|---|------|
| acc cag tcc gcc ctg agc aaa gac ccc aac gag aag cgc gat cac atg | 1488 |
| Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met | |
| 485 490 495 | |
| | |
| gtc ctg ctg gag ttc gtg acc gcc gcc ggg atc act ctc ggc atg gac | 1536 |
| Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp | |
| 500 505 510 | |
| | |
| gag ctg tac aag atg tct act gtc cac gaa atc ctg tgc aag ctc agc | 1584 |
| Glu Leu Tyr Lys Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser | |
| 515 520 525 | |
| | |
| ttg gag ggt gtt cat tct aca ccc cca agt gcc gga tcc | 1623 |
| Leu Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser | |
| 530 535 540 | |

<210> 34
 <211> 541
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 YFP-NLS-CP3-multiple DEVD-CFP-Annexin II construct

<400> 34
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|
| Gly | Ile | Lys | Val | Asn | Phe | Lys | Ile | Arg | His | Asn | Ile | Glu | Asp | Gly | Ser | | |
| | | | | 165 | | | | | 170 | | | | | 175 | | | |
| Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn | Thr | Pro | Ile | Gly | Asp | Gly | | |
| | | | 180 | | | | | 185 | | | | | 190 | | | | |
| Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | Tyr | Gln | Ser | Ala | Leu | | |
| | | 195 | | | | | 200 | | | | | 205 | | | | | |
| Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu | Leu | Glu | Phe | | |
| | 210 | | | | | 215 | | | | 220 | | | | | | | |
| Val | Thr | Ala | Ala | Gly | Ile | Thr | Leu | Gly | Met | Asp | Glu | Leu | Tyr | Lys | Ser | | |
| 225 | | | | | 230 | | | | | 235 | | | | | 240 | | |
| Gly | Arg | Arg | Lys | Arg | Gln | Lys | Arg | Ser | Ala | Gly | Asp | Glu | Val | Asp | Ala | | |
| | | | | 245 | | | | | 250 | | | | | 255 | | | |
| Gly | Asp | Glu | Val | Asp | Ala | Gly | Asp | Glu | Val | Asp | Ala | Gly | Asp | Glu | Val | | |
| | | | 260 | | | | | 265 | | | | | 270 | | | | |
| Asp | Ala | Gly | Ser | Thr | Met | Val | Ser | Lys | Gly | Glu | Glu | Leu | Phe | Thr | Gly | | |
| | | 275 | | | | | 280 | | | | | 285 | | | | | |
| Val | Val | Pro | Ile | Leu | Val | Glu | Leu | Asp | Gly | Asp | Val | Asn | Gly | His | Lys | | |
| | | 290 | | | | 295 | | | | | 300 | | | | | | |
| Phe | Ser | Val | Ser | Gly | Glu | Gly | Glu | Gly | Asp | Ala | Thr | Tyr | Gly | Lys | Leu | | |
| 305 | | | | | 310 | | | | 315 | | | | | | 320 | | |
| Thr | Leu | Lys | Phe | Ile | Cys | Thr | Thr | Gly | Lys | Leu | Pro | Val | Pro | Trp | Pro | | |
| | | | | 325 | | | | | 330 | | | | | 335 | | | |
| Thr | Leu | Val | Thr | Thr | Leu | Thr | Trp | Gly | Val | Gln | Cys | Phe | Ser | Arg | Tyr | | |
| | | | 340 | | | | | 345 | | | | | 350 | | | | |
| Pro | Asp | His | Met | Lys | Gln | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro | Glu | | |
| | | 355 | | | | | 360 | | | | | 365 | | | | | |
| Gly | Tyr | Val | Gln | Glu | Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn | Tyr | | |
| | 370 | | | | | 375 | | | | | 380 | | | | | | |
| Lys | Thr | Arg | Ala | Glu | Val | Lys | Phe | Glu | Gly | Asp | Thr | Leu | Val | Asn | Arg | | |
| 385 | | | | | 390 | | | | | 395 | | | | | 400 | | |
| Ile | Glu | Leu | Lys | Gly | Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu | Gly | | |
| | | | | 405 | | | | | 410 | | | | 415 | | | | |
| His | Lys | Leu | Glu | Tyr | Asn | Tyr | Ile | Ser | His | Asn | Val | Tyr | Ile | Thr | Ala | | |
| | | | 420 | | | | | 425 | | | | | 430 | | | | |
| Asp | Lys | Gln | Lys | Asn | Gly | Ile | Lys | Ala | Asn | Phe | Lys | Ile | Arg | His | Asn | | |
| | | 435 | | | | | 440 | | | | | 445 | | | | | |
| Ile | Glu | Asp | Gly | Ser | Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn | Thr | | |
| | 450 | | | | | 455 | | | | | 460 | | | | | | |

Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser
 465 470 475 480

Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met
 485 490 495

Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp
 500 505 510

Glu Leu Tyr Lys Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser
 515 520 525

Leu Glu Gly Val His Ser Thr Pro Pro Ser Ala Gly Ser
 530 535 540

<210> 35
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FLAG epitope

<400> 35
 gactacaaag acgacgacga caaa

24

<210> 36
 <211> 8
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: FLAG epitope

<400> 36
 Asp Tyr Lys Asp Asp Asp Asp Lys
 1 5

<210> 37
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: HA epitope

<400> 37
 tacccatacg acgtaccaga ctacgca

27

<210> 38
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HA epitope

<400> 38
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1 5

<210> 39
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: KT3 epitope

<400> 39
ccaccagaac cagaaaca

18

<210> 40
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: KT3 epitope

<400> 40
Pro Pro Glu Pro Glu Thr
1 5

<210> 41
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Myc epitope

<400> 41
gcagaagaac aaaaattaat aagcgaagaa gactta

36

<210> 42
<211> 12
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Myc epitope

<400> 42
Ala Glu Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
1 5 10

<210> 43
 <211> 717
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(717)

<220>
 <223> Description of Artificial Sequence: EYFP

<400> 43

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | gtg | agc | aag | ggc | gag | gag | ctg | ttc | acc | ggg | gtg | gtg | ccc | atc | ctg | 48 |
| Met | Val | Ser | Lys | Gly | Glu | Glu | Leu | Phe | Thr | Gly | Val | Val | Pro | Ile | Leu | |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | | |
| | | | | | | | | | | | | | | | | |
| gtc | gag | ctg | gac | ggc | gac | gta | aac | ggc | cac | aag | ttc | agc | gtg | tcc | ggc | 96 |
| Val | Glu | Leu | Asp | Gly | Asp | Val | Asn | Gly | His | Lys | Phe | Ser | Val | Ser | Gly | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| | | | | | | | | | | | | | | | | |
| gag | ggc | gag | ggc | gat | gcc | acc | tac | ggc | aag | ctg | acc | ctg | aag | ttc | atc | 144 |
| Glu | Gly | Glu | Gly | Asp | Ala | Thr | Tyr | Gly | Lys | Leu | Thr | Leu | Lys | Phe | Ile | |
| | | | 35 | | | | | 40 | | | | | 45 | | | |
| | | | | | | | | | | | | | | | | |
| tgc | acc | acc | ggc | aag | ctg | ccc | gtg | ccc | tgg | ccc | acc | ctc | gtg | acc | acc | 192 |
| Cys | Thr | Thr | Gly | Lys | Leu | Pro | Val | Pro | Trp | Pro | Thr | Leu | Val | Thr | Thr | |
| | | | 50 | | | | 55 | | | | 60 | | | | | |
| | | | | | | | | | | | | | | | | |
| ttc | ggc | tac | ggc | ctg | cag | tgc | ttc | gcc | cgc | tac | ccc | gac | cac | atg | aag | 240 |
| Phe | Gly | Tyr | Gly | Leu | Gln | Cys | Phe | Ala | Arg | Tyr | Pro | Asp | His | Met | Lys | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | |
| | | | | | | | | | | | | | | | | |
| cag | cac | gac | ttc | ttc | aag | tcc | gcc | atg | ccc | gaa | ggc | tac | gtc | cag | gag | 288 |
| Gln | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro | Glu | Gly | Tyr | Val | Gln | Glu | |
| | | | | | 85 | | | | 90 | | | | | 95 | | |
| | | | | | | | | | | | | | | | | |
| cgc | acc | atc | ttc | ttc | aag | gac | gac | ggc | aac | tac | aag | acc | cgc | gcc | gag | 336 |
| Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn | Tyr | Lys | Thr | Arg | Ala | Glu | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| | | | | | | | | | | | | | | | | |
| gtg | aag | ttc | gag | ggc | gac | acc | ctg | gtg | aac | cgc | atc | gag | ctg | aag | ggc | 384 |
| Val | Lys | Phe | Glu | Gly | Asp | Thr | Leu | Val | Asn | Arg | Ile | Glu | Leu | Lys | Gly | |
| | | | 115 | | | | 120 | | | | | 125 | | | | |
| | | | | | | | | | | | | | | | | |
| atc | gac | ttc | aag | gag | gac | ggc | aac | atc | ctg | ggg | cac | aag | ctg | gag | tac | 432 |
| Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu | Gly | His | Lys | Leu | Glu | Tyr | |
| | | | 130 | | | | 135 | | | | 140 | | | | | |
| | | | | | | | | | | | | | | | | |
| aac | tac | aac | agc | cac | aac | gtc | tat | atc | atg | gcc | gac | aag | cag | aag | aac | 480 |
| Asn | Tyr | Asn | Ser | His | Asn | Val | Tyr | Ile | Met | Ala | Asp | Lys | Gln | Lys | Asn | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| | | | | | | | | | | | | | | | | |
| ggc | atc | aag | gtg | aac | ttc | aag | atc | cgc | cac | aac | atc | gag | gac | ggc | agc | 528 |
| Gly | Ile | Lys | Val | Asn | Phe | Lys | Ile | Arg | His | Asn | Ile | Glu | Asp | Gly | Ser | |

| 165 | | | | | | | | | | 170 | | | | | | | | | | 175 | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|--|--|--|-----|--|--|--|--|--|--|--|--|--|--|
| gtg | cag | ctc | gcc | gac | cac | tac | cag | cag | aac | acc | ccc | atc | ggc | gac | ggc | 576 | | | | | | | | | | | | | | |
| Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn | Thr | Pro | Ile | Gly | Asp | Gly | | | | | | | | | | | | | | | |
| 180 | | | | | 185 | | | | | 190 | | | | | | | | | | | | | | | | | | | | |
| ccc | gtg | ctg | ctg | ccc | gac | aac | cac | tac | ctg | agc | tac | cag | tcc | gcc | ctg | 624 | | | | | | | | | | | | | | |
| Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | Tyr | Gln | Ser | Ala | Leu | | | | | | | | | | | | | | | |
| 195 | | | | | 200 | | | | | 205 | | | | | | | | | | | | | | | | | | | | |
| agc | aaa | gac | ccc | aac | gag | aag | cgc | gat | cac | atg | gtc | ctg | ctg | gag | ttc | 672 | | | | | | | | | | | | | | |
| Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu | Leu | Glu | Phe | | | | | | | | | | | | | | | |
| 210 | | | | | 215 | | | | | 220 | | | | | | | | | | | | | | | | | | | | |
| gtg | acc | gcc | gcc | ggg | atc | act | ctc | ggc | atg | gac | gag | ctg | tac | aag | 717 | | | | | | | | | | | | | | | |
| Val | Thr | Ala | Ala | Gly | Ile | Thr | Leu | Gly | Met | Asp | Glu | Leu | Tyr | Lys | | | | | | | | | | | | | | | | |
| 225 | | | | | 230 | | | | | 235 | | | | | | | | | | | | | | | | | | | | |

<210> 44
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: EYFP

<400> 44

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Met | Val | Ser | Lys | Gly | Glu | Glu | Leu | Phe | Thr | Gly | Val | Val | Pro | Ile | Leu |
| 1 | | | | 5 | | | | | 10 | | | | | 15 | |
| Val | Glu | Leu | Asp | Gly | Asp | Val | Asn | Gly | His | Lys | Phe | Ser | Val | Ser | Gly |
| | | | 20 | | | | | 25 | | | | | 30 | | |
| Glu | Gly | Glu | Gly | Asp | Ala | Thr | Tyr | Gly | Lys | Leu | Thr | Leu | Lys | Phe | Ile |
| | | | 35 | | | | 40 | | | | | | 45 | | |
| Cys | Thr | Thr | Gly | Lys | Leu | Pro | Val | Pro | Trp | Pro | Thr | Leu | Val | Thr | Thr |
| | 50 | | | | | 55 | | | | | 60 | | | | |
| Phe | Gly | Tyr | Gly | Leu | Gln | Cys | Phe | Ala | Arg | Tyr | Pro | Asp | His | Met | Lys |
| 65 | | | | | 70 | | | | | 75 | | | | | 80 |
| Gln | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro | Glu | Gly | Tyr | Val | Gln | Glu |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn | Tyr | Lys | Thr | Arg | Ala | Glu |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Val | Lys | Phe | Glu | Gly | Asp | Thr | Leu | Val | Asn | Arg | Ile | Glu | Leu | Lys | Gly |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu | Gly | His | Lys | Leu | Glu | Tyr |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Asn | Tyr | Asn | Ser | His | Asn | Val | Tyr | Ile | Met | Ala | Asp | Lys | Gln | Lys | Asn |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 45
<211> 717
<212> DNA
<213> Artificial Sequence

<220>
<221> CDS
<222> (1)..(717)

<220>
<223> Description of Artificial Sequence: EGFP

<400> 45
atg gtg agc aag ggc gag gag ctg ttc acc ggg gtg gtg ccc atc ctg 48
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

B1

| | |
|---|-----|
| gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc | 384 |
| Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly | |
| 115 120 125 | |
| atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac | 432 |
| Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr | |
| 130 135 140 | |
| aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac | 480 |
| Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn | |
| 145 150 155 160 | |
| ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc | 528 |
| Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser | |
| 165 170 175 | |
| gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc | 576 |
| Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly | |
| 180 185 190 | |
| ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg | 624 |
| Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu | |
| 195 200 205 | |
| agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc | 672 |
| Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe | |
| 210 215 220 | |
| gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag | 717 |
| Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys | |
| 225 230 235 | |

<210> 46
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: EGFP

<400> 46
 Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

<210> 47

<220>

<220>

<400> 47

gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

| | |
|---|-----|
| tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc | 192 |
| Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr | |
| 50 55 60 | |
| ctg acc cac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag | 240 |
| Leu Thr His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys | |
| 65 70 75 80 | |
| cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag | 288 |
| Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu | |
| 85 90 95 | |
| cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag | 336 |
| Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu | |
| 100 105 110 | |
| gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc | 384 |
| Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly | |
| 115 120 125 | |
| atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac | 432 |
| Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr | |
| 130 135 140 | |
| aac ttc aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac | 480 |
| Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn | |
| 145 150 155 160 | |
| ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc | 528 |
| Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser | |
| 165 170 175 | |
| gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc | 576 |
| Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly | |
| 180 185 190 | |
| ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg | 624 |
| Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu | |
| 195 200 205 | |
| agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc | 672 |
| Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe | |
| 210 215 220 | |
| gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag | 717 |
| Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys | |
| 225 230 235 | |

<210> 48

<211> 239

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: EBFP

<400> 48

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
Leu Thr His Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
Asn Phe Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 49

<211> 717

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1) .. (717)

<220>

<223> Description of Artificial Sequence: ECFP

<400> 49

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| atg | gtg | agc | aag | ggc | gag | gag | ctg | ttc | acc | ggg | gtg | gtg | ccc | atc | ctg | 48 |
| Met | Val | Ser | Lys | Gly | Glu | Glu | Leu | Phe | Thr | Gly | Val | Val | Pro | Ile | Leu | |
| 1 | | | | 5 | | | | 10 | | | | | 15 | | | |
| gtc | gag | ctg | gac | ggc | gac | gta | aac | ggc | cac | aag | ttc | agc | gtg | tcc | ggc | 96 |
| Val | Glu | Leu | Asp | Gly | Asp | Val | Asn | Gly | His | Lys | Phe | Ser | Val | Ser | Gly | |
| | | | 20 | | | | | 25 | | | | | 30 | | | |
| gag | ggc | gag | ggc | gat | gcc | acc | tac | ggc | aag | ctg | acc | ctg | aag | ttc | atc | 144 |
| Glu | Gly | Glu | Gly | Asp | Ala | Thr | Tyr | Gly | Lys | Leu | Thr | Leu | Lys | Phe | Ile | |
| | | 35 | | | | | 40 | | | | | 45 | | | | |
| tgc | acc | acc | ggc | aag | ctg | ccc | gtg | ccc | tgg | ccc | acc | ctc | gtg | acc | acc | 192 |
| Cys | Thr | Thr | Gly | Lys | Leu | Pro | Val | Pro | Trp | Pro | Thr | Leu | Val | Thr | Thr | |
| | 50 | | | | | 55 | | | | | 60 | | | | | |
| ctg | acc | tgg | ggc | gtg | cag | tgc | ttc | agc | cgc | tac | ccc | gac | cac | atg | aag | 240 |
| Leu | Thr | Trp | Gly | Val | Gln | Cys | Phe | Ser | Arg | Tyr | Pro | Asp | His | Met | Lys | |
| 65 | | | | | 70 | | | | 75 | | | | | | 80 | |
| cag | cac | gac | ttc | ttc | aag | tcc | gcc | atg | ccc | gaa | ggc | tac | gtc | cag | gag | 288 |
| Gln | His | Asp | Phe | Phe | Lys | Ser | Ala | Met | Pro | Glu | Gly | Tyr | Val | Gln | Glu | |
| | | | 85 | | | | | | 90 | | | | | 95 | | |
| cgc | acc | atc | ttc | ttc | aag | gac | gac | ggc | aac | tac | aag | acc | cgc | gcc | gag | 336 |
| Arg | Thr | Ile | Phe | Phe | Lys | Asp | Asp | Gly | Asn | Tyr | Lys | Thr | Arg | Ala | Glu | |
| | | | 100 | | | | | 105 | | | | | 110 | | | |
| gtg | aag | ttc | gag | ggc | gac | acc | ctg | gtg | aac | cgc | atc | gag | ctg | aag | ggc | 384 |
| Val | Lys | Phe | Glu | Gly | Asp | Thr | Leu | Val | Asn | Arg | Ile | Glu | Leu | Lys | Gly | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| atc | gac | ttc | aag | gag | gac | ggc | aac | atc | ctg | ggg | cac | aag | ctg | gag | tac | 432 |
| Ile | Asp | Phe | Lys | Glu | Asp | Gly | Asn | Ile | Leu | Gly | His | Lys | Leu | Glu | Tyr | |
| | 130 | | | | | 135 | | | | | 140 | | | | | |
| aac | tac | atc | agc | cac | aac | gtc | tat | atc | acc | gcc | gac | aag | cag | aag | aac | 480 |
| Asn | Tyr | Ile | Ser | His | Asn | Val | Tyr | Ile | Thr | Ala | Asp | Lys | Gln | Lys | Asn | |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 | |
| ggc | atc | aag | gcc | aac | ttc | aag | atc | cgc | cac | aac | atc | gag | gac | ggc | agc | 528 |
| Gly | Ile | Lys | Ala | Asn | Phe | Lys | Ile | Arg | His | Asn | Ile | Glu | Asp | Gly | Ser | |
| | | | 165 | | | | | 170 | | | | | | 175 | | |
| gtg | cag | ctc | gcc | gac | cac | tac | cag | cag | aac | acc | ccc | atc | ggc | gac | ggc | 576 |
| Val | Gln | Leu | Ala | Asp | His | Tyr | Gln | Gln | Asn | Thr | Pro | Ile | Gly | Asp | Gly | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| ccc | gtg | ctg | ctg | ccc | gac | aac | cac | tac | ctg | agc | acc | cag | tcc | gcc | ctg | 624 |
| Pro | Val | Leu | Leu | Pro | Asp | Asn | His | Tyr | Leu | Ser | Thr | Gln | Ser | Ala | Leu | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| agc | aaa | gac | ccc | aac | gag | aag | cgc | gat | cac | atg | gtc | ctg | ctg | gag | ttc | 672 |
| Ser | Lys | Asp | Pro | Asn | Glu | Lys | Arg | Asp | His | Met | Val | Leu | Leu | Glu | Phe | |

210 215 220 717

gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg' tac aag
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
225 230 235

<210> 50
<211> 239
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: ECFP

<400> 50
Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
1 5 10 15
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160
Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 225 230 235

<210> 51
 <211> 720
 <212> DNA
 <213> Artificial Sequence

<220>
 <221> CDS
 <222> (1)..(717)

<220>
 <223> Description of Artificial Sequence: Fred25

<400> 51
 atg gct agc aaa gga gaa gaa ctc ttc act gga gtt gtc cca att ctt 48
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 gtt gaa tta gat ggt gat gtt aac ggc cac aag ttc tct gtc agt gga 96
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 gag ggt gaa ggt gat gca aca tac gga aaa ctt acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 tgc act act ggc aaa ctg cct gtt cca tgg cca aca cta gtc act act 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 ctg tgc tat ggt gtt caa tgc ttt tca aga tac ccg gat cat atg aaa 240
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 cgg cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa 288
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 agg acc atc ttc ttc aaa gat gac ggc aac tac aag aca cgt gct gaa 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtc aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 att gac ttc aag gaa gat ggc aac att ctg gga cac aaa ttg gaa tac 432
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac tat aac tca cac aat gta tac atc atg gca gac aaa caa aag aat 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

| | |
|---|-----|
| gga atc aaa gtg aac ttc aag acc cgc cac aac att gaa gat gga agc | 528 |
| Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser | |
| 165 170 175 | |
| | |
| gtt caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc | 576 |
| Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly | |
| 180 185 190 | |
| | |
| cct gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt | 624 |
| Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu | |
| 195 200 205 | |
| | |
| tcg aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt | 672 |
| Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe | |
| 210 215 220 | |
| | |
| gta aca gct gct ggg att aca cat ggc atg gat gaa ctg tac aac tag | 720 |
| Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn | |
| 225 230 235 | |

<210> 52
 <211> 239
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fred25

<400> 52
 Met Ala Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
 1 5 10 15
 Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
 20 25 30
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60
 Leu Cys Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80
 Arg His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

B1

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 Gly Ile Lys Val Asn Phe Lys Thr Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220
 Val Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Asn
 225 230 235

<210> 53
 <211> 14
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Caspase-1,4,5
 substrate recognition sequence

<400> 53
 tgggaacatg acaa

14

<210> 54
 <211> 4
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Caspase-1,4,5
 substrate recognition sequence

<400> 54
 Trp Glu His Asp
 1

<210> 55
 <211> 12
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: proCaspase-1
 substrate recognition sequence

<400> 55

tggttttaaag ac

12

<210> 56

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: proCaspase-1
substrate recognition sequence

<400> 56

Trp Phe Lys Asp

1

<210> 57

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-2
substrate recognition sequence

<400> 57

gacgaacacg ac

12

<210> 58

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-2
substrate recognition sequence

<400> 58

Asp Glu His Asp

1

<210> 59

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-3,7
substrate recognition sequence

<400> 59

gacgaagttg ac

12

<210> 60
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-3,7
substrate recognition sequence

<400> 60
Asp Glu Val Asp
1

<210> 61
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-3
substrate recognition sequence

<400> 61
atagaaacag ac

12

<210> 62
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-3
substrate recognition sequence

<400> 62
Ile Glu Thr Asp
1

<210> 63
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-4,5
substrate recognition sequence

<400> 63
tgggtaagag ac

12

<210> 64
<211> 4
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: proCaspase-4,5
substrate recognition sequence

<400> 64

Trp Val Arg Asp

1

<210> 65

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 65

gtagaaatag ac

12

<210> 66

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 66

Val Glu Ile Asp

1

<210> 67

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 67

gtagaacacg ac

12

<210> 68

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

B1

<223> Description of Artificial Sequence: Caspase-6
substrate recognition sequence

<400> 68
Val Glu His Asp
1

<210> 69
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-6
substrate recognition sequence

<400> 69
acagaagtag ac

12

<210> 70
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-6
substrate recognition sequence

<400> 70
Thr Glu Val Asp
1

<210> 71
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-7
substrate recognition sequence

<400> 71
atacaagcag ac

12

<210> 72
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-7
substrate recognition sequence

<400> 72
Ile Gln Ala Asp
1

<210> 73
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-8
substrate recognition sequence

<400> 73
gtagaaacag ac

12

<210> 74
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-8
substrate recognition sequence

<400> 74
Val Glu Thr Asp
1

<210> 75
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-8
substrate recognition sequence

<400> 75
ttagaaacag ac

12

<210> 76
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-8
substrate recognition sequence

<400> 76
Leu Glu Thr Asp
1

B1

<210> 77
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-9
substrate recognition sequence

<400> 77
ttagaacacg ac

12

<210> 78
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-9
substrate recognition sequence

<400> 78
Leu Glu His Asp
1

<210> 79
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-9
substrate recognition sequence

<400> 79
ttagaacacg ac

12

<210> 80
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: proCaspase-9
substrate recognition sequence

<400> 80
Leu Glu His Asp
1

<210> 81

B1

<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 81
agccaaaatt ac

12

<210> 82
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 82
Ser Gln Asn Tyr
1

<210> 83
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 83
ccaatagtac aa

12

<210> 84
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: HIV protease
substrate recognition sequence

<400> 84
Pro Ile Val Gln
1

<210> 85
<211> 12
<212> DNA
<213> Artificial Sequence

b1

<220>

<223> Description of Artificial Sequence: Adenovirus
 endopeptidase substrate recognition sequence

<400> 85

atgtttggag ga

12

<210> 86

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Adenovirus
 endopeptidase substrate recognition sequence

<400> 86

Met Phe Gly Gly

1

<210> 87

<211> 12

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Adenovirus
 endopeptidase substrate recognition sequence

<400> 87

gcaaaaaaaaa ga

12

<210> 88

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Adenovirus
 endopeptidase substrate recognition sequence

<400> 88

Ala Lys Lys Arg

1

<210> 89

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: b-Secretase

b1

substrate recognition sequence

<400> 89
gtgaaaatg

9

<210> 90
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: b-Secretase
substrate recognition sequence

<400> 90
Val Lys Met
1

<210> 91
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: b-Secretase
substrate recognition sequence

<400> 91
gacgcagaat tc

12

<210> 92
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: b-Secretase
substrate recognition sequence

<400> 92
Asp Ala Glu Phe
1

<210> 93
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Cathepsin D
substrate recognition sequence

<400> 93

aaaccagcat tattc

15

<210> 94

<211> 5

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cathepsin D
substrate recognition sequence

<400> 94

Lys Pro Ala Leu Phe

1

5

<210> 95

<211> 9

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cathepsin D
substrate recognition sequence

<400> 95

ttcagatta

9

<210> 96

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Cathepsin D
substrate recognition sequence

<400> 96

Phe Arg Leu

1

<210> 97

<211> 15

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Matrix
Metalloprotease substrate recognition sequence

<400> 97

ggaccattag gacca

15

bl

<210> 98
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Matrix
Metalloprotease substrate recognition sequence

<400> 98
Gly Pro Leu Gly Pro
1 5

<210> 99
<211> 12
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Granzyme B
substrate recognition sequence

<400> 99
atagaaccag ac

12

<210> 100
<211> 4
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Granzyme B
substrate recognition sequence

<400> 100
Ile Glu Pro Asp
1

<210> 101
<211> 36
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Anthrax
protease substrate recognition sequence

<400> 101
atgcccaaga agaagccgac gcccatccag ctgaac

36

<210> 102
<211> 12
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Anthrax
protease substrate recognition sequence

<400> 102

Met Pro Lys Lys Lys Pro Thr Pro Ile Gln Leu Asn
1 5 10

<210> 103

<211> 45

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Anthrax
protease substrate recognition sequence

<400> 103

atgctggccc ggaggaagcc ggtgctgccg gcgctcacca tcaac

45

<210> 104

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Anthrax
protease substrate recognition sequence

<400> 104

Met Leu Ala Arg Arg Lys Pro Val Leu Pro Ala Leu Thr Ile Asn
1 5 10 15

<210> 105

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
tetanus/botulium substrate recognition sequence

<400> 105

gcctcgcagt ttgaaaca

18

<210> 106

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
tetanus/botulium substrate recognition sequence

<400> 106
Ala Ser Gln Phe Glu Thr
1 5

<210> 107
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
tetanus/botulium substrate recognition sequence

<400> 107
gcttctcaat ttgaaacg

18

<210> 108
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
tetanus/botulium substrate recognition sequence

<400> 108
Ala Ser Gln Phe Glu Thr
1 5

<210> 109
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin A substrate recognition sequence

<400> 109
gccaaccaac gtgcaaca

18

<210> 110
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin A substrate recognition sequence

<400> 110
Ala Asn Gln Arg Ala Thr
1 5

<210> 111
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin B substrate recognition sequence

<400> 111
gcttctcaat ttgaaacg

18

<210> 112
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin B substrate recognition sequence

<400> 112
Ala Ser Gln Phe Glu Thr
1 5

<210> 113
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin C substrate recognition sequence

<400> 113
acgaaaaaag ctgtgaaa

18

<210> 114
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin C substrate recognition sequence

<400> 114
Thr Lys Lys Ala Val Lys
1 5

B1

<210> 115
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin D substrate recognition sequence

<400> 115
gaccagaagc tctctgag

18

<210> 116
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin D substrate recognition sequence

<400> 116
Asp Gln Lys Leu Ser Glu
1 5

<210> 117
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin E substrate recognition sequence

<400> 117
atcgacagga tcatggag

18

<210> 118
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Botulinum
neurotoxin E substrate recognition sequence

<400> 118
Ile Asp Arg Ile Met Glu
1 5

<210> 119

<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Botulinum
neurotoxin F substrate recognition sequence

<400> 119
agagaccaga agctctct

18

<210> 120
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Botulinum
neurotoxin F substrate recognition sequence

<400> 120
Arg Asp Gln Lys Leu Ser
1 5

<210> 121
<211> 18
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Botulinum
neurotoxin G substrate recognition sequence

<400> 121
acgagcgcag ccaagttg

18

<210> 122
<211> 6
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Botulinum
neurotoxin G substrate recognition sequence

<400> 122
Thr Ser Ala Ala Lys Leu
1 5

<210> 123
<211> 69
<212> DNA
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Cytoplasm/cytoskeleton target sequence

<400> 123

atgtctactg tccacgaaat cctgtgcaag ctcagcttgg aggggtgttca ttctacaccc 60

ccaagtgcc

69

<210> 124

<211> 23

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
Cytoplasm/cytoskeleton target sequence

<400> 124

Met Ser Thr Val His Glu Ile Leu Cys Lys Leu Ser Leu Glu Gly Val
1 5 10 15

His Ser Thr Pro Pro Ser Ala
20

<210> 125

<211> 96

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Inner surface
of plasma membrane target sequence

<400> 125

atgggatgta cattaagcgc agaagacaaa gcagcagtag aaagaagcaa aatgatagac 60

agaaacttaa gagaagacgg agaaaaagct gctaga

96

<210> 126

<211> 32

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Inner surface
of plasma membrane target sequence

<400> 126

Met Gly Cys Thr Leu Ser Ala Glu Asp Lys Ala Ala Val Glu Arg Ser
1 5 10 15

Lys Met Ile Asp Arg Asn Leu Arg Glu Asp Gly Glu Lys Ala Ala Arg

<210> 127
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Nucleus target
 sequence

<400> 127
 agaaggaac gacaaaag 18

<210> 128
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Nucleus target
 sequence

<400> 128
 Arg Arg Lys Arg Gln Lys
 1 5

<210> 129
 <211> 90
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Nucleolus
 target sequence

<400> 129
 agaaaacgta tacgtactta cctcaagtcc tgcaggcgga tgaaaagaag tggttttgag 60
 atgtctcgac ctattccttc ccaccttact 90

<210> 130
 <211> 30
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Nucleolus
 target sequence

B1

<400> 130

Arg Lys Arg Ile Arg Thr Tyr Leu Lys Ser Cys Arg Arg Met Lys Arg
1 5 10 15

Ser Gly Phe Glu Met Ser Arg Pro Ile Pro Ser His Leu Thr
20 25 30

<210> 131

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mitochondria
target sequence

<400> 131

atgtccgtcc tgacgccgct gctgctgcgg ggcttgacag gtcgggccg gcggctccca 60

gtgccgcgcg ccaagatcca ttcgttg 87

<210> 132

<211> 29

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Mitochondria
target sequence

<400> 132

Met Ser Val Leu Thr Pro Leu Leu Leu Arg Gly Leu Thr Gly Ser Ala
1 5 10 15

Arg Arg Leu Pro Val Pro Arg Ala Leu Ile His Ser Leu
20 25

<210> 133

<211> 99

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nuclear
Envelope target sequence

<400> 133

atgagcattg ttttaataat tgttattgtg gtgatttttt taatatgttt tttatattta 60

agcaacagca aagatcccag agtaccagtt gaattaatg 99

<210> 134

<211> 33

<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nuclear
Envelope target sequence

<400> 134
Met Ser Ile Val Leu Ile Ile Val Ile Val Val Ile Phe Leu Ile Cys
1 5 10 15

Phe Leu Tyr Leu Ser Asn Ser Lys Asp Pro Arg Val Pro Val Glu Leu
20 25 30

Met

<210> 135
<211> 246
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Golgi target
sequence

<400> 135
atgaggcttc gggagccgct cctgagcggc agcgccgcga tgccaggcgc gtccttacag 60
cgggcctgcc gcctgctcgt ggccgtctgc gctctgcacc ttggcgtcac cctcgtttac 120
tacctggctg gccgcgacct gagccgcctg ccccaactgg tcggagtctc cacaccgctg 180
cagggcggct cgaacagtgc cgccgccatc gggcagtcct ccggggagct ccggaccgga 240
ggggcc 246

<210> 136
<211> 82
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Golgi target
sequence

<400> 136
Met Arg Leu Arg Glu Pro Leu Leu Ser Gly Ser Ala Ala Met Pro Gly
1 5 10 15

Ala Ser Leu Gln Arg Ala Cys Arg Leu Leu Val Ala Val Cys Ala Leu
20 25 30

His Leu Gly Val Thr Leu Val Tyr Tyr Leu Ala Gly Arg Asp Leu Ser
35 40 45

Arg Leu Pro Gln Leu Val Gly Val Ser Thr Pro Leu Gln Gly Gly Ser
 50 55 60

Asn Ser Ala Ala Ala Ile Gly Gln Ser Ser Gly Glu Leu Arg Thr Gly
 65 70 75 80

Gly Ala

<210> 137
 <211> 150
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Endoplasmic
 reticulum target sequence

<400> 137
 gaaacaataa gacctataag aataagaaga tgttcttatt ttacatctac agacagcaaa 60
 atggcaattc aattaagatc tccctttcca ttagcattac caggaatggt agctttatta 120
 ggatgggtggt ggtttttcag tagaaaaaaa 150

<210> 138
 <211> 50
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Endoplasmic
 reticulum target sequence

<400> 138
 Glu Thr Ile Arg Pro Ile Arg Ile Arg Arg Cys Ser Tyr Phe Thr Ser
 1 5 10 15
 Thr Asp Ser Lys Met Ala Ile Gln Leu Arg Ser Pro Phe Pro Leu Ala
 20 25 30
 Leu Pro Gly Met Leu Ala Leu Leu Gly Trp Trp Trp Phe Phe Ser Arg
 35 40 45
 Lys Lys
 50

b1
 <210> 139
 <211> 39
 <212> DNA
 <213> Artificial Sequence
 <220>

<223> Description of Artificial Sequence: Nuclear Export
target sequence

<400> 139

gccttgacaga agaagctgga ggagctagag cttgatgag

39

<210> 140

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Nuclear Export
target sequence

<400> 140

Ala Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu
1 5 10

<210> 141

<211> 1024

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Size exclusion
target sequence

<400> 141

gccgacctca gtcttggtga tgcgttgaca gaaccacctc cagaaattga gggagaaata 60
aagcgagact tcatggctgc gctggaggca gagccctatg atgacatcgt gggagaaact 120
gtggagaaaa ctgagtttat tcctctcctg gatggtgatg agaaaaccgg gaactcagag 180
tccaaaaaga aaccctgctt agacactagc cagggttgaag gtatcccatc ttctaaacca 240
acactcctag ccaatggtga tcatggaatg gaggggaata aactgcagg gtctccaact 300
gacttccttg aagagagagt ggactatccg gattatcaga gcagccagaa ctggccagaa 360
gatgcaagct tttgtttcca gcctcagcaa gtgtagata ctgaccaggc tgagcccttt 420
aacgagcacc gtgatgatgg tttggcagat ctgctctttg tctccagtgg acccacgaac 480
gcttctgcat ttacagagcg agacaatcct tcagaagaca gttacggtat gcttcctgt 540
gactcatttg cttccacggc tgttgatctt caggagtggc ctgtgggagc cccaaactct 600
ccatgttcag agtcctgtgt ctccccagag gttactatag aaaccctaca gccagcaaca 660
gagctctcca aggcagcaga agtggaatca gtgaaagagc agctgccagc taaagcattg 720
gaaacgatgg cagagcagac cactgatgtg gtgcactctc catccacaga cacaacacca 780

ggcccagaca cagaggcagc actggctaaa gacatagaag agatcaccaa gccagatgtg 840
atattggcaa atgtcacgca gccatctact gaatcgata tgttcctggc ccaggacatg 900
gaactactca caggaacaga ggcagccac gctaacaata tcatattgcc tacagaacca 960
gacgaatctt caaccaagga tgtagcacca cctatggaag aagaaattgt cccaggcaat 1020
gata 1024

<210> 142
<211> 566
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Size exclusion
target sequence

<400> 142
Ala Asp Leu Ser Leu Val Asp Ala Leu Thr Glu Pro Pro Pro Glu Ile
1 5 10 15
Glu Gly Glu Ile Lys Arg Asp Phe Met Ala Ala Leu Glu Ala Glu Pro
20 25 30
Tyr Asp Asp Ile Val Gly Glu Thr Val Glu Lys Thr Glu Phe Ile Pro
35 40 45
Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn Ser Glu Ser Lys Lys Lys
50 55 60
Pro Cys Leu Asp Thr Ser Gln Val Glu Gly Ile Pro Ser Ser Lys Pro
65 70 75 80
Thr Leu Leu Ala Asn Gly Asp His Gly Met Glu Gly Asn Asn Thr Ala
85 90 95
Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg Val Asp Tyr Pro Asp Tyr
100 105 110
Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala Ser Phe Cys Phe Gln Pro
115 120 125
Gln Gln Val Leu Asp Thr Asp Gln Ala Glu Pro Phe Asn Glu His Arg
130 135 140
Asp Asp Gly Leu Ala Asp Leu Leu Phe Val Ser Ser Gly Pro Thr Asn
145 150 155 160
Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro Ser Glu Asp Ser Tyr Gly
165 170 175
Met Leu Pro Cys Asp Ser Phe Ala Ser Thr Ala Val Val Ser Gln Glu
180 185 190

Trp Ser Val Gly Ala Pro Asn Ser Pro Cys Ser Glu Ser Cys Val Ser
 195 200 205
 Pro Glu Val Thr Ile Glu Thr Leu Gln Pro Ala Thr Glu Leu Ser Lys
 210 215 220
 Ala Ala Glu Val Glu Ser Val Lys Glu Gln Leu Pro Ala Lys Ala Leu
 225 230 235 240
 Glu Thr Met Ala Glu Gln Thr Thr Asp Val Val His Ser Pro Ser Thr
 245 250 255
 Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala Ala Leu Ala Lys Asp Ile
 260 265 270
 Glu Glu Ile Thr Lys Pro Asp Val Ile Leu Ala Asn Val Thr Gln Pro
 275 280 285
 Ser Thr Glu Ser Asp Met Phe Leu Ala Gln Asp Met Glu Leu Leu Thr
 290 295 300
 Gly Thr Glu Ala Ala His Ala Asn Asn Ile Ile Leu Pro Thr Glu Pro
 305 310 315 320
 Asp Glu Ser Ser Thr Lys Asp Val Ala Pro Pro Met Glu Glu Glu Ile
 325 330 335
 Val Pro Gly Asn Asp Thr Thr Ser Pro Lys Glu Thr Glu Thr Thr Leu
 340 345 350
 Pro Ile Lys Met Asp Leu Ala Pro Pro Glu Asp Val Leu Leu Thr Lys
 355 360 365
 Glu Thr Glu Leu Ala Pro Ala Lys Gly Met Val Ser Leu Ser Glu Ile
 370 375 380
 Glu Glu Ala Leu Ala Lys Asn Asp Val Arg Ser Ala Glu Ile Pro Val
 385 390 395 400
 Ala Gln Glu Thr Val Val Ser Glu Thr Glu Val Val Leu Ala Thr Glu
 405 410 415
 Val Val Leu Pro Ser Asp Pro Ile Thr Thr Leu Thr Lys Asp Val Thr
 420 425 430
 Leu Pro Leu Glu Ala Glu Arg Pro Leu Val Thr Asp Met Thr Pro Ser
 435 440 445
 Leu Glu Thr Glu Met Thr Leu Gly Lys Glu Thr Ala Pro Pro Thr Glu
 450 455 460
 Thr Asn Leu Gly Met Ala Lys Asp Met Ser Pro Leu Pro Glu Ser Glu
 465 470 475 480
 Val Thr Leu Gly Lys Asp Val Val Ile Leu Pro Glu Thr Lys Val Ala
 485 490 495

Glu Phe Asn Asn Val Thr Pro Leu Ser Glu Glu Glu Val Thr Ser Val
500 505 510

Lys Asp Met Ser Pro Ser Ala Glu Thr Glu Ala Pro Leu Ala Lys Asn
515 520 525

Ala Asp Leu His Ser Gly Thr Glu Leu Ile Val Asp Asn Ser Met Ala
530 535 540

Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu Thr Lys Val Ala Thr Val
545 550 555 560

Pro Ile Lys Asp Lys Gly
565

<210> 143
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Vesicle
membrane target sequence

<400> 143
atgtgggcaa tcgggattac tggtctgggtt atcttcatca tcatcatcat cgtgtggggtt 60
gtc 63

<210> 144
<211> 21
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Vesicle
membrane target sequence

<400> 144
Met Trp Ala Ile Gly Ile Thr Val Leu Val Ile Phe Ile Ile Ile Ile
1 5 10 15

Ile Val Trp Val Val
20

<210> 145
<211> 61
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Vesicle
membrane target sequence

B1

<400> 145
atgtgggcga tagggatcag tgtcctgggtg atcattgtca tcatcatcat cgtgtgggtgt 60

g

61

<210> 146
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Vesicle
membrane target sequence

<400> 146
Met Trp Ala Ile Gly Ile Ser Val Leu Val Ile Ile Val Ile Ile Ile
1 5 10 15

Ile Val Trp Cys
20

<210> 147
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nuclear Export
target sequence

<400> 147
gacctgcaga agaagctgga ggagctggaa cttgacgag 39

<210> 148
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Nuclear Export
target sequence

<400> 148
Asp Leu Gln Lys Lys Leu Glu Glu Leu Glu Leu Asp Glu
1 5 10

b1
<210> 149
<211> 9
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Peroxisome

target sequence

<400> 149

tctaaactg

9

<210> 150

<211> 3

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Peroxisome
target sequence

<400> 150

Ser Lys Leu

1

<210> 151

<211> 3378

<212> DNA

<213> Mus musculus

<220>

<221> CDS

<222> (1)..(3375)

<400> 151

| | |
|---|----|
| atg gcc gac ctc agt ctt gtg gat gcg ttg aca gaa cca cct cca gaa | 48 |
| Met Ala Asp Leu Ser Leu Val Asp Ala Leu Thr Glu Pro Pro Pro Glu | |
| 1 5 10 15 | |

| | |
|---|----|
| att gag gga gaa ata aag cga gac ttc atg gct gcg ctg gag gca gag | 96 |
| Ile Glu Gly Glu Ile Lys Arg Asp Phe Met Ala Ala Leu Glu Ala Glu | |
| 20 25 30 | |

| | |
|---|-----|
| ccc tat gat gac atc gtg gga gaa act gtg gag aaa act gag ttt att | 144 |
| Pro Tyr Asp Asp Ile Val Gly Glu Thr Val Glu Lys Thr Glu Phe Ile | |
| 35 40 45 | |

| | |
|---|-----|
| cct ctc ctg gat ggt gat gag aaa acc ggg aac tca gag tcc aaa aag | 192 |
| Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn Ser Glu Ser Lys Lys | |
| 50 55 60 | |

| | |
|---|-----|
| aaa ccc tgc tta gac act agc cag gtt gaa ggt atc cca tct tct aaa | 240 |
| Lys Pro Cys Leu Asp Thr Ser Gln Val Glu Gly Ile Pro Ser Ser Lys | |
| 65 70 75 80 | |

B1

| | |
|---|-----|
| cca aca ctc cta gcc aat ggt gat cat gga atg gag ggg aat aac act | 288 |
| Pro Thr Leu Leu Ala Asn Gly Asp His Gly Met Glu Gly Asn Asn Thr | |
| 85 90 95 | |

| | |
|---|-----|
| gca ggg tct cca act gac ttc ctt gaa gag aga gtg gac tat ccg gat | 336 |
| Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg Val Asp Tyr Pro Asp | |
| 100 105 110 | |

| | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|
| tat | cag | agc | agc | cag | aac | tgg | cca | gaa | gat | gca | agc | ttt | tgt | ttc | cag | 384 |
| Tyr | Gln | Ser | Ser | Gln | Asn | Trp | Pro | Glu | Asp | Ala | Ser | Phe | Cys | Phe | Gln | |
| | | 115 | | | | | 120 | | | | | 125 | | | | |
| cct | cag | caa | gtg | tta | gat | act | gac | cag | gct | gag | ccc | ttt | aac | gag | cac | 432 |
| Pro | Gln | Gln | Val | Leu | Asp | Thr | Asp | Gln | Ala | Glu | Pro | Phe | Asn | Glu | His | |
| | | 130 | | | | 135 | | | | | 140 | | | | | |
| cgt | gat | gat | ggg | ttg | gca | gat | ctg | ctc | ttt | gtc | tcc | agt | gga | ccc | acg | 480 |
| Arg | Asp | Asp | Gly | Leu | Ala | Asp | Leu | Leu | Phe | Val | Ser | Ser | Gly | Pro | Thr | |
| | | | | | | 150 | | | | 155 | | | | | 160 | |
| aac | gct | tct | gca | ttt | aca | gag | cga | gac | aat | cct | tca | gaa | gac | agt | tac | 528 |
| Asn | Ala | Ser | Ala | Phe | Thr | Glu | Arg | Asp | Asn | Pro | Ser | Glu | Asp | Ser | Tyr | |
| | | | | 165 | | | | | 170 | | | | | 175 | | |
| ggg | atg | ctt | ccc | tgt | gac | tca | ttt | gct | tcc | acg | gct | gtt | gta | tct | cag | 576 |
| Gly | Met | Leu | Pro | Cys | Asp | Ser | Phe | Ala | Ser | Thr | Ala | Val | Val | Ser | Gln | |
| | | | 180 | | | | | 185 | | | | | 190 | | | |
| gag | tgg | tct | gtg | gga | gcc | cca | aac | tct | cca | tgt | tca | gag | tcc | tgt | gtc | 624 |
| Glu | Trp | Ser | Val | Gly | Ala | Pro | Asn | Ser | Pro | Cys | Ser | Glu | Ser | Cys | Val | |
| | | 195 | | | | | 200 | | | | | 205 | | | | |
| tcc | cca | gag | gtt | act | ata | gaa | acc | cta | cag | cca | gca | aca | gag | ctc | tcc | 672 |
| Ser | Pro | Glu | Val | Thr | Ile | Glu | Thr | Leu | Gln | Pro | Ala | Thr | Glu | Leu | Ser | |
| | | 210 | | | | | 215 | | | | 220 | | | | | |
| aag | gca | gca | gaa | gtg | gaa | tca | gtg | aaa | gag | cag | ctg | cca | gct | aaa | gca | 720 |
| Lys | Ala | Ala | Glu | Val | Glu | Ser | Val | Lys | Glu | Gln | Leu | Pro | Ala | Lys | Ala | |
| | | | | | | 230 | | | | 235 | | | | | 240 | |
| ttg | gaa | acg | atg | gca | gag | cag | acc | act | gat | gtg | gtg | cac | tct | cca | tcc | 768 |
| Leu | Glu | Thr | Met | Ala | Glu | Gln | Thr | Thr | Asp | Val | Val | His | Ser | Pro | Ser | |
| | | | | 245 | | | | | 250 | | | | | 255 | | |
| aca | gac | aca | aca | cca | ggc | cca | gac | aca | gag | gca | gca | ctg | gct | aaa | gac | 816 |
| Thr | Asp | Thr | Thr | Pro | Gly | Pro | Asp | Thr | Glu | Ala | Ala | Leu | Ala | Lys | Asp | |
| | | | | 260 | | | | 265 | | | | | 270 | | | |
| ata | gaa | gag | atc | acc | aag | cca | gat | gtg | ata | ttg | gca | aat | gtc | acg | cag | 864 |
| Ile | Glu | Glu | Ile | Thr | Lys | Pro | Asp | Val | Ile | Leu | Ala | Asn | Val | Thr | Gln | |
| | | | 275 | | | | 280 | | | | | 285 | | | | |
| cca | tct | act | gaa | tcg | gat | atg | ttc | ctg | gcc | cag | gac | atg | gaa | cta | ctc | 912 |
| Pro | Ser | Thr | Glu | Ser | Asp | Met | Phe | Leu | Ala | Gln | Asp | Met | Glu | Leu | Leu | |
| | | | 290 | | | | 295 | | | | 300 | | | | | |
| aca | gga | aca | gag | gca | gcc | cac | gct | aac | aat | atc | ata | ttg | cct | aca | gaa | 960 |
| Thr | Gly | Thr | Glu | Ala | Ala | His | Ala | Asn | Asn | Ile | Ile | Leu | Pro | Thr | Glu | |
| | | | | | 310 | | | | | 315 | | | | | 320 | |
| cca | gac | gaa | tct | tca | acc | aag | gat | gta | gca | cca | cct | atg | gaa | gaa | gaa | 1008 |
| Pro | Asp | Glu | Ser | Ser | Thr | Lys | Asp | Val | Ala | Pro | Pro | Met | Glu | Glu | Glu | |
| | | | | 325 | | | | | 330 | | | | | 335 | | |

| | |
|---|------|
| att gtc cca ggc aat gat acg aca tcc ccc aaa gaa aca gag aca aca | 1056 |
| Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys Glu Thr Glu Thr Thr | |
| 340 345 350 | |
| ctt cca ata aaa atg gac ttg gca cca cct gag gat gtg tta ctt acc | 1104 |
| Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu Asp Val Leu Leu Thr | |
| 355 360 365 | |
| aaa gaa aca gaa cta gcc cca gcc aag ggc atg gtt tca ctc tca gaa | 1152 |
| Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met Val Ser Leu Ser Glu | |
| 370 375 380 | |
| ata gaa gag gct ctg gca aag aat gat gtt cgc tct gca gaa ata cct | 1200 |
| Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg Ser Ala Glu Ile Pro | |
| 385 390 395 400 | |
| gtg gct cag gag aca gtg gtc tca gaa aca gag gtg gtc ctg gca aca | 1248 |
| Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu Val Val Leu Ala Thr | |
| 405 410 415 | |
| gaa gtg gta ctg ccc tca gat ccc ata aca aca ttg aca aag gat gtg | 1296 |
| Glu Val Val Leu Pro Ser Asp Pro Ile Thr Thr Leu Thr Lys Asp Val | |
| 420 425 430 | |
| aca ctc ccc tta gaa gca gag aga ccg ttg gtg acg gac atg act cca | 1344 |
| Thr Leu Pro Leu Glu Ala Glu Arg Pro Leu Val Thr Asp Met Thr Pro | |
| 435 440 445 | |
| tct ctg gaa aca gaa atg acc cta ggc aaa gag aca gct cca ccc aca | 1392 |
| Ser Leu Glu Thr Glu Met Thr Leu Gly Lys Glu Thr Ala Pro Pro Thr | |
| 450 455 460 | |
| gaa aca aat ttg ggc atg gcc aaa gac atg tct cca ctc cca gaa tca | 1440 |
| Glu Thr Asn Leu Gly Met Ala Lys Asp Met Ser Pro Leu Pro Glu Ser | |
| 465 470 475 480 | |
| gaa gtg act ctg ggc aag gac gtg gtt ata ctt cca gaa aca aag gtg | 1488 |
| Glu Val Thr Leu Gly Lys Asp Val Val Ile Leu Pro Glu Thr Lys Val | |
| 485 490 495 | |
| gct gag ttt aac aat gtg act cca ctt tca gaa gaa gag gta acc tca | 1536 |
| Ala Glu Phe Asn Asn Val Thr Pro Leu Ser Glu Glu Glu Val Thr Ser | |
| 500 505 510 | |
| gtc aag gac atg tct ccg tct gca gaa aca gag gct ccc ctg gct aag | 1584 |
| Val Lys Asp Met Ser Pro Ser Ala Glu Thr Glu Ala Pro Leu Ala Lys | |
| 515 520 525 | |
| aat gct gat ctg cac tca gga aca gag ctg att gtg gac aac agc atg | 1632 |
| Asn Ala Asp Leu His Ser Gly Thr Glu Leu Ile Val Asp Asn Ser Met | |
| 530 535 540 | |
| gct cca gcc tcc gat ctt gca ctg ccc ttg gaa aca aaa gta gca aca | 1680 |
| Ala Pro Ala Ser Asp Leu Ala Leu Pro Leu Glu Thr Lys Val Ala Thr | |
| 545 550 555 560 | |
| gtt cca att aaa gac aaa gga act gta cag act gaa gaa aaa cca cgt | 1728 |

B1

| | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|------|--|
| Val | Pro | Ile | Lys | Asp | Lys | Gly | Thr | Val | Gln | Thr | Glu | Glu | Lys | Pro | Arg | | |
| | | | | 565 | | | | | 570 | | | | | 575 | | | |
| gaa | gac | tcc | cag | tta | gca | tct | atg | cag | cac | aag | gga | cag | tca | aca | gta | 1776 | |
| Glu | Asp | Ser | Gln | Leu | Ala | Ser | Met | Gln | His | Lys | Gly | Gln | Ser | Thr | Val | | |
| | | | 580 | | | | | 585 | | | | 590 | | | | | |
| cct | cct | tgc | acg | gct | tca | cca | gaa | cca | gtc | aaa | gct | gca | gaa | caa | atg | 1824 | |
| Pro | Pro | Cys | Thr | Ala | Ser | Pro | Glu | Pro | Val | Lys | Ala | Ala | Glu | Gln | Met | | |
| | | 595 | | | | | 600 | | | | | 605 | | | | | |
| tct | acc | tta | cca | ata | gat | gca | cct | tct | cca | tta | gag | aac | tta | gag | cag | 1872 | |
| Ser | Thr | Leu | Pro | Ile | Asp | Ala | Pro | Ser | Pro | Leu | Glu | Asn | Leu | Glu | Gln | | |
| | 610 | | | | | 615 | | | | | 620 | | | | | | |
| aag | gaa | acg | cct | ggc | agc | cag | cct | tct | gag | cct | tgc | tca | gga | gta | tcc | 1920 | |
| Lys | Glu | Thr | Pro | Gly | Ser | Gln | Pro | Ser | Glu | Pro | Cys | Ser | Gly | Val | Ser | | |
| 625 | | | | | 630 | | | | 635 | | | | | | 640 | | |
| cgg | caa | gaa | gaa | gca | aag | gct | gct | gta | ggg | gtg | act | gga | aat | gac | atc | 1968 | |
| Arg | Gln | Glu | Glu | Ala | Lys | Ala | Ala | Val | Gly | Val | Thr | Gly | Asn | Asp | Ile | | |
| | | | | 645 | | | | | 650 | | | | | 655 | | | |
| act | acc | ccg | cca | aac | aag | gag | cca | cca | cca | agc | cca | gaa | aag | aaa | gca | 2016 | |
| Thr | Thr | Pro | Pro | Asn | Lys | Glu | Pro | Pro | Pro | Ser | Pro | Glu | Lys | Lys | Ala | | |
| | | | 660 | | | | | 665 | | | | | 670 | | | | |
| aag | cct | ttg | gcc | acc | act | caa | cct | gca | aag | act | tca | aca | tcg | aaa | gcc | 2064 | |
| Lys | Pro | Leu | Ala | Thr | Thr | Gln | Pro | Ala | Lys | Thr | Ser | Thr | Ser | Lys | Ala | | |
| | | 675 | | | | | 680 | | | | | 685 | | | | | |
| aaa | aca | cag | ccc | act | tct | ctc | cct | aag | caa | cca | gct | ccc | acc | acc | tct | 2112 | |
| Lys | Thr | Gln | Pro | Thr | Ser | Leu | Pro | Lys | Gln | Pro | Ala | Pro | Thr | Thr | Ser | | |
| | 690 | | | | | 695 | | | | | 700 | | | | | | |
| ggg | ggg | ttg | aat | aaa | aaa | ccc | atg | agc | ctc | gcc | tca | ggc | tca | gtg | cca | 2160 | |
| Gly | Gly | Leu | Asn | Lys | Lys | Pro | Met | Ser | Leu | Ala | Ser | Gly | Ser | Val | Pro | | |
| 705 | | | | | 710 | | | | | 715 | | | | | 720 | | |
| gct | gcc | cca | cac | aaa | cgc | cct | gct | gct | gcc | act | gct | act | gcc | agg | cct | 2208 | |
| Ala | Ala | Pro | His | Lys | Arg | Pro | Ala | Ala | Ala | Thr | Ala | Thr | Ala | Arg | Pro | | |
| | | | | 725 | | | | | 730 | | | | | 735 | | | |
| tcc | acc | cta | cct | gcc | aga | gac | gtg | aag | cca | aag | cca | att | aca | gaa | gct | 2256 | |
| Ser | Thr | Leu | Pro | Ala | Arg | Asp | Val | Lys | Pro | Lys | Pro | Ile | Thr | Glu | Ala | | |
| | | | 740 | | | | | 745 | | | | | 750 | | | | |
| aag | gtt | gcc | gaa | aag | cgg | acc | tct | cca | tcc | aag | cct | tca | tct | gcc | cca | 2304 | |
| Lys | Val | Ala | Glu | Lys | Arg | Thr | Ser | Pro | Ser | Lys | Pro | Ser | Ser | Ala | Pro | | |
| | | 755 | | | | | 760 | | | | | 765 | | | | | |
| gcc | ctc | aaa | cct | gga | cct | aaa | acc | acc | cca | acc | gtt | tca | aaa | gcc | aca | 2352 | |
| Ala | Leu | Lys | Pro | Gly | Pro | Lys | Thr | Thr | Pro | Thr | Val | Ser | Lys | Ala | Thr | | |
| | | 770 | | | | 775 | | | | | 780 | | | | | | |
| tct | ccc | tca | act | ctt | gtt | tcc | act | gga | cca | agt | agt | aga | agt | cca | gct | 2400 | |
| Ser | Pro | Ser | Thr | Leu | Val | Ser | Thr | Gly | Pro | Ser | Ser | Arg | Ser | Pro | Ala | | |

B1

| 785 | 790 | | | | | | | 795 | | | | | | | 800 | | | | | | | |
|---|---|------|------|-----|--|--|--|-----|--|--|--|--|--|--|-----|--|--|--|--|--|--|--|
| aca act ctg cct aag agg cca acc agc atc aag act gag ggg aaa cct | Thr Thr Leu Pro Lys Arg Pro Thr Ser Ile Lys Thr Glu Gly Lys Pro | 2448 | | | | | | | | | | | | | | | | | | | | |
| | 805 | 810 | 815 | | | | | | | | | | | | | | | | | | | |
| gct gat gtc aaa agg atg act gct aag tct gcc tca gct gac ttg agt | Ala Asp Val Lys Arg Met Thr Ala Lys Ser Ala Ser Ala Asp Leu Ser | 2496 | | | | | | | | | | | | | | | | | | | | |
| | 820 | 825 | 830 | | | | | | | | | | | | | | | | | | | |
| cgc tca aag acc acc tct gcc agt tct gtg aag aga aac acc act ccc | Arg Ser Lys Thr Thr Ser Ala Ser Ser Val Lys Arg Asn Thr Thr Pro | 2544 | | | | | | | | | | | | | | | | | | | | |
| | 835 | 840 | 845 | | | | | | | | | | | | | | | | | | | |
| act ggg gca gca ccc cca gca ggg atg act tcc act cga gtc aag ccc | Thr Gly Ala Ala Pro Pro Ala Gly Met Thr Ser Thr Arg Val Lys Pro | 2592 | | | | | | | | | | | | | | | | | | | | |
| | 850 | 855 | 860 | | | | | | | | | | | | | | | | | | | |
| atg tct gca cct agc cgc tct tct ggg gct ctt tct gtg gac aag aag | Met Ser Ala Pro Ser Arg Ser Ser Gly Ala Leu Ser Val Asp Lys Lys | 2640 | | | | | | | | | | | | | | | | | | | | |
| | 865 | 870 | 875 | 880 | | | | | | | | | | | | | | | | | | |
| ccc act tcc act aag cct agc tcc tct gct ccc agg gtg agc cgc ctg | Pro Thr Ser Thr Lys Pro Ser Ser Ser Ala Pro Arg Val Ser Arg Leu | 2688 | | | | | | | | | | | | | | | | | | | | |
| | 885 | 890 | 895 | | | | | | | | | | | | | | | | | | | |
| gcc aca act gtt tct gcc cct gac ctg aag agt gtt cgc tcc aag gtc | Ala Thr Thr Val Ser Ala Pro Asp Leu Lys Ser Val Arg Ser Lys Val | 2736 | | | | | | | | | | | | | | | | | | | | |
| | 900 | 905 | 910 | | | | | | | | | | | | | | | | | | | |
| ggc tct aca gaa aac atc aaa cac cag cct gga gga ggc cgg gcc aaa | Gly Ser Thr Glu Asn Ile Lys His Gln Pro Gly Gly Gly Arg Ala Lys | 2784 | | | | | | | | | | | | | | | | | | | | |
| | 915 | 920 | 925 | | | | | | | | | | | | | | | | | | | |
| gta gag aaa aaa aca gag gca gct acc aca gct ggg aag cct gaa cct | Val Glu Lys Lys Thr Glu Ala Ala Thr Thr Ala Gly Lys Pro Glu Pro | 2832 | | | | | | | | | | | | | | | | | | | | |
| | 930 | 935 | 940 | | | | | | | | | | | | | | | | | | | |
| aat gca gtc act aaa gca gcc ggc tcc att gcg agt gca cag aaa ccg | Asn Ala Val Thr Lys Ala Ala Gly Ser Ile Ala Ser Ala Gln Lys Pro | 2880 | | | | | | | | | | | | | | | | | | | | |
| | 945 | 950 | 955 | 960 | | | | | | | | | | | | | | | | | | |
| cct gct ggg aaa gtc cag ata gta tcc aaa aaa gtg agc tac agt cat | Pro Ala Gly Lys Val Gln Ile Val Ser Lys Lys Val Ser Tyr Ser His | 2928 | | | | | | | | | | | | | | | | | | | | |
| | 965 | 970 | 975 | | | | | | | | | | | | | | | | | | | |
| att caa tcc aag tgt gtt tcc aag gac aat att aag cat gtc cct gga | Ile Gln Ser Lys Cys Val Ser Lys Asp Asn Ile Lys His Val Pro Gly | 2976 | | | | | | | | | | | | | | | | | | | | |
| | 980 | 985 | 990 | | | | | | | | | | | | | | | | | | | |
| tgt ggc aat gtt cag att cag aac aag aaa gtg gac ata tcc aag gtc | Cys Gly Asn Val Gln Ile Gln Asn Lys Lys Val Asp Ile Ser Lys Val | 3024 | | | | | | | | | | | | | | | | | | | | |
| | 995 | 1000 | 1005 | | | | | | | | | | | | | | | | | | | |
| tcc tcc aag tgt ggg tcc aaa gct aat atc aag cac aag cct ggt gga | Ser Ser Lys Cys Gly Ser Lys Ala Asn Ile Lys His Lys Pro Gly Gly | 3072 | | | | | | | | | | | | | | | | | | | | |
| | 1010 | 1015 | 1020 | | | | | | | | | | | | | | | | | | | |

gga gat gtc aag att gaa agt cag aag ttg aac ttc aag gag aag gcc 3120
 Gly Asp Val Lys Ile Glu Ser Gln Lys Leu Asn Phe Lys Glu Lys Ala
 1025 1030 1035 1040

caa gcc aaa gtg gga tcc ctt gat aac gtt ggc cac ttt cct gca gga 3168
 Gln Ala Lys Val Gly Ser Leu Asp Asn Val Gly His Phe Pro Ala Gly
 1045 1050 1055

ggt gcc gtg aag act gag ggc ggt ggc agt gag gcc ctt ccg tgt cca 3216
 Gly Ala Val Lys Thr Glu Gly Gly Gly Ser Glu Ala Leu Pro Cys Pro
 1060 1065 1070

ggc ccc ccc gct ggg gag gag cca gtc atc cct gag gct gcg cct gac 3264
 Gly Pro Pro Ala Gly Glu Glu Pro Val Ile Pro Glu Ala Ala Pro Asp
 1075 1080 1085

cgt ggc gcc cct act tca gcc agt ggc ctc agt ggc cac acc acc ctg 3312
 Arg Gly Ala Pro Thr Ser Ala Ser Gly Leu Ser Gly His Thr Thr Leu
 1090 1095 1100

tca ggg ggt ggt gac caa agg gag ccc cag acc ttg gac agc cag atc 3360
 Ser Gly Gly Gly Asp Gln Arg Glu Pro Gln Thr Leu Asp Ser Gln Ile
 1105 1110 1115 1120

cag gag aca agc atc taa 3378
 Gln Glu Thr Ser Ile
 1125

<210> 152
 <211> 1125
 <212> PRT
 <213> Mus musculus

<400> 152
 Met Ala Asp Leu Ser Leu Val Asp Ala Leu Thr Glu Pro Pro Pro Glu
 1 5 10 15

Ile Glu Gly Glu Ile Lys Arg Asp Phe Met Ala Ala Leu Glu Ala Glu
 20 25 30

Pro Tyr Asp Asp Ile Val Gly Glu Thr Val Glu Lys Thr Glu Phe Ile
 35 40 45

Pro Leu Leu Asp Gly Asp Glu Lys Thr Gly Asn Ser Glu Ser Lys Lys
 50 55 60

Lys Pro Cys Leu Asp Thr Ser Gln Val Glu Gly Ile Pro Ser Ser Lys
 65 70 75 80

Pro Thr Leu Leu Ala Asn Gly Asp His Gly Met Glu Gly Asn Asn Thr
 85 90 95

Ala Gly Ser Pro Thr Asp Phe Leu Glu Glu Arg Val Asp Tyr Pro Asp
 100 105 110

B1

Tyr Gln Ser Ser Gln Asn Trp Pro Glu Asp Ala Ser Phe Cys Phe Gln
 115 120 125
 Pro Gln Gln Val Leu Asp Thr Asp Gln Ala Glu Pro Phe Asn Glu His
 130 135 140
 Arg Asp Asp Gly Leu Ala Asp Leu Leu Phe Val Ser Ser Gly Pro Thr
 145 150 155 160
 Asn Ala Ser Ala Phe Thr Glu Arg Asp Asn Pro Ser Glu Asp Ser Tyr
 165 170 175
 Gly Met Leu Pro Cys Asp Ser Phe Ala Ser Thr Ala Val Val Ser Gln
 180 185 190
 Glu Trp Ser Val Gly Ala Pro Asn Ser Pro Cys Ser Glu Ser Cys Val
 195 200 205
 Ser Pro Glu Val Thr Ile Glu Thr Leu Gln Pro Ala Thr Glu Leu Ser
 210 215 220
 Lys Ala Ala Glu Val Glu Ser Val Lys Glu Gln Leu Pro Ala Lys Ala
 225 230 235 240
 Leu Glu Thr Met Ala Glu Gln Thr Thr Asp Val Val His Ser Pro Ser
 245 250 255
 Thr Asp Thr Thr Pro Gly Pro Asp Thr Glu Ala Ala Leu Ala Lys Asp
 260 265 270
 Ile Glu Glu Ile Thr Lys Pro Asp Val Ile Leu Ala Asn Val Thr Gln
 275 280 285
 Pro Ser Thr Glu Ser Asp Met Phe Leu Ala Gln Asp Met Glu Leu Leu
 290 295 300
 Thr Gly Thr Glu Ala Ala His Ala Asn Asn Ile Ile Leu Pro Thr Glu
 305 310 315 320
 Pro Asp Glu Ser Ser Thr Lys Asp Val Ala Pro Pro Met Glu Glu Glu
 325 330 335
 Ile Val Pro Gly Asn Asp Thr Thr Ser Pro Lys Glu Thr Glu Thr Thr
 340 345 350
 Leu Pro Ile Lys Met Asp Leu Ala Pro Pro Glu Asp Val Leu Leu Thr
 355 360 365
 Lys Glu Thr Glu Leu Ala Pro Ala Lys Gly Met Val Ser Leu Ser Glu
 370 375 380
 Ile Glu Glu Ala Leu Ala Lys Asn Asp Val Arg Ser Ala Glu Ile Pro
 385 390 395 400
 Val Ala Gln Glu Thr Val Val Ser Glu Thr Glu Val Val Leu Ala Thr
 405 410 415

| | | | | | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Glu | Val | Val | Leu | Pro | Ser | Asp | Pro | Ile | Thr | Thr | Leu | Thr | Lys | Asp | Val | 420 | 425 | 430 | |
| Thr | Leu | Pro | Leu | Glu | Ala | Glu | Arg | Pro | Leu | Val | Thr | Asp | Met | Thr | Pro | 435 | 440 | 445 | |
| Ser | Leu | Glu | Thr | Glu | Met | Thr | Leu | Gly | Lys | Glu | Thr | Ala | Pro | Pro | Thr | 450 | 455 | 460 | |
| Glu | Thr | Asn | Leu | Gly | Met | Ala | Lys | Asp | Met | Ser | Pro | Leu | Pro | Glu | Ser | 465 | 470 | 475 | 480 |
| Glu | Val | Thr | Leu | Gly | Lys | Asp | Val | Val | Ile | Leu | Pro | Glu | Thr | Lys | Val | 485 | 490 | 495 | |
| Ala | Glu | Phe | Asn | Asn | Val | Thr | Pro | Leu | Ser | Glu | Glu | Glu | Val | Thr | Ser | 500 | 505 | 510 | |
| Val | Lys | Asp | Met | Ser | Pro | Ser | Ala | Glu | Thr | Glu | Ala | Pro | Leu | Ala | Lys | 515 | 520 | 525 | |
| Asn | Ala | Asp | Leu | His | Ser | Gly | Thr | Glu | Leu | Ile | Val | Asp | Asn | Ser | Met | 530 | 535 | 540 | |
| Ala | Pro | Ala | Ser | Asp | Leu | Ala | Leu | Pro | Leu | Glu | Thr | Lys | Val | Ala | Thr | 545 | 550 | 555 | 560 |
| Val | Pro | Ile | Lys | Asp | Lys | Gly | Thr | Val | Gln | Thr | Glu | Glu | Lys | Pro | Arg | 565 | 570 | 575 | |
| Glu | Asp | Ser | Gln | Leu | Ala | Ser | Met | Gln | His | Lys | Gly | Gln | Ser | Thr | Val | 580 | 585 | 590 | |
| Pro | Pro | Cys | Thr | Ala | Ser | Pro | Glu | Pro | Val | Lys | Ala | Ala | Glu | Gln | Met | 595 | 600 | 605 | |
| Ser | Thr | Leu | Pro | Ile | Asp | Ala | Pro | Ser | Pro | Leu | Glu | Asn | Leu | Glu | Gln | 610 | 615 | 620 | |
| Lys | Glu | Thr | Pro | Gly | Ser | Gln | Pro | Ser | Glu | Pro | Cys | Ser | Gly | Val | Ser | 625 | 630 | 635 | 640 |
| Arg | Gln | Glu | Glu | Ala | Lys | Ala | Ala | Val | Gly | Val | Thr | Gly | Asn | Asp | Ile | 645 | 650 | 655 | |
| Thr | Thr | Pro | Pro | Asn | Lys | Glu | Pro | Pro | Pro | Ser | Pro | Glu | Lys | Lys | Ala | 660 | 665 | 670 | |
| Lys | Pro | Leu | Ala | Thr | Thr | Gln | Pro | Ala | Lys | Thr | Ser | Thr | Ser | Lys | Ala | 675 | 680 | 685 | |
| Lys | Thr | Gln | Pro | Thr | Ser | Leu | Pro | Lys | Gln | Pro | Ala | Pro | Thr | Thr | Ser | 690 | 695 | 700 | |
| Gly | Gly | Leu | Asn | Lys | Lys | Pro | Met | Ser | Leu | Ala | Ser | Gly | Ser | Val | Pro | 705 | 710 | 715 | 720 |

Ala Ala Pro His Lys Arg Pro Ala Ala Ala Thr Ala Thr Ala Arg Pro
 725 730 735
 Ser Thr Leu Pro Ala Arg Asp Val Lys Pro Lys Pro Ile Thr Glu Ala
 740 745 750
 Lys Val Ala Glu Lys Arg Thr Ser Pro Ser Lys Pro Ser Ser Ala Pro
 755 760 765
 Ala Leu Lys Pro Gly Pro Lys Thr Thr Pro Thr Val Ser Lys Ala Thr
 770 775 780
 Ser Pro Ser Thr Leu Val Ser Thr Gly Pro Ser Ser Arg Ser Pro Ala
 785 790 795 800
 Thr Thr Leu Pro Lys Arg Pro Thr Ser Ile Lys Thr Glu Gly Lys Pro
 805 810 815
 Ala Asp Val Lys Arg Met Thr Ala Lys Ser Ala Ser Ala Asp Leu Ser
 820 825 830
 Arg Ser Lys Thr Thr Ser Ala Ser Ser Val Lys Arg Asn Thr Thr Pro
 835 840 845
 Thr Gly Ala Ala Pro Pro Ala Gly Met Thr Ser Thr Arg Val Lys Pro
 850 855 860
 Met Ser Ala Pro Ser Arg Ser Ser Gly Ala Leu Ser Val Asp Lys Lys
 865 870 875 880
 Pro Thr Ser Thr Lys Pro Ser Ser Ser Ala Pro Arg Val Ser Arg Leu
 885 890 895
 Ala Thr Thr Val Ser Ala Pro Asp Leu Lys Ser Val Arg Ser Lys Val
 900 905 910
 Gly Ser Thr Glu Asn Ile Lys His Gln Pro Gly Gly Gly Arg Ala Lys
 915 920 925
 Val Glu Lys Lys Thr Glu Ala Ala Thr Thr Ala Gly Lys Pro Glu Pro
 930 935 940
 Asn Ala Val Thr Lys Ala Ala Gly Ser Ile Ala Ser Ala Gln Lys Pro
 945 950 955 960
 Pro Ala Gly Lys Val Gln Ile Val Ser Lys Lys Val Ser Tyr Ser His
 965 970 975
 Ile Gln Ser Lys Cys Val Ser Lys Asp Asn Ile Lys His Val Pro Gly
 980 985 990
 Cys Gly Asn Val Gln Ile Gln Asn Lys Lys Val Asp Ile Ser Lys Val
 995 1000 1005
 Ser Ser Lys Cys Gly Ser Lys Ala Asn Ile Lys His Lys Pro Gly Gly
 1010 1015 1020

Gly Asp Val Lys Ile Glu Ser Gln Lys Leu Asn Phe Lys Glu Lys Ala
 1025 1030 1035 1040
 Gln Ala Lys Val Gly Ser Leu Asp Asn Val Gly His Phe Pro Ala Gly
 1045 1050 1055
 Gly Ala Val Lys Thr Glu Gly Gly Gly Ser Glu Ala Leu Pro Cys Pro
 1060 1065 1070
 Gly Pro Pro Ala Gly Glu Glu Pro Val Ile Pro Glu Ala Ala Pro Asp
 1075 1080 1085
 Arg Gly Ala Pro Thr Ser Ala Ser Gly Leu Ser Gly His Thr Thr Leu
 1090 1095 1100
 Ser Gly Gly Gly Asp Gln Arg Glu Pro Gln Thr Leu Asp Ser Gln Ile
 1105 1110 1115 1120
 Gln Glu Thr Ser Ile
 1125

<210> 153
 <211> 96
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 153
 tcatcatccg gagctggagc cggagctggc cgatcggctg ttaaactctga aggaaagaga 60
 aagtgtgacg aagttgatgg aattgatgaa gtagca 96

<210> 154
 <211> 99
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 oligonucleotide

<400> 154
 gaagaaggat ccggcacttg ggggtgtaga atgaacaccc tccaagctga gcttgcacag 60
 gatttcgtgg acagtagaca tagtacttgc tacttcac 99

<210> 155
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 155

tcatcatccg gagctgga

18

<210> 156

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 156

gaagaaggat ccggcact

18

<210> 157

<211> 96

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 157

tcatcatccg gaagaaggaa acgacaaaag cgatcggctg ttaaactctga aggaaagaga 60

aagtgtgacg aagttgatgg aattgatgaa gtagca

96

<210> 158

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 158

tcatcatccg gaagaagg

18

<210> 159

<211> 60

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 159
tcatcatccg gaagaaggaa acgacaaaag cgatcgacaa gacttggtga aattgacaac 60

<210> 160
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 160
gaagaaggat ccggcacttg ggggtgtaga atgaacaccc tccaagctga gcttgcacag 60
gatttcgtgg acagtagaca tagtactggt gtcaatttc 99

<210> 161
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 161
tcatcatccg gaagaaggaa acgacaaaag cgatcgatc aaaaaggaat accagttgaa 60
acagacagcg aagagcaacc ttat 84

<210> 162
<211> 99
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 162
gaagaaggat ccggcacttg ggggtgtaga atgaacaccc tccaagctga gcttgcacag 60
gatttcgtgg acagtagaca tagtactata aggttgctc 99

<210> 163
<211> 60
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

oligonucleotide

<400> 163
tcatcatccg gaagaaaacg tatacgtact tacctcaagt cctgcaggcg gatgaaaaga 60

<210> 164
<211> 63
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 164
gaagaacgat cgagtaaggt gggaaggaat aggtcgagac atctcaaaac cacttctttt 60
cat 63

<210> 165
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 165
tcatcatccg gaagaaaa 18

<210> 166
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
oligonucleotide

<400> 166
gaagaacgat cgagtaag 18

<210> 167
<211> 14
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Caspase-1,4,5
substrate recognition sequence

<400> 167

ttagaacatg acaa

14

<210> 168

<211> 4

<212> PRT

<213> Artificial Sequence

*BI
Concld* <220>

<223> Description of Artificial Sequence: Caspase-1,4,5
substrate recognition sequence

<400> 168

Leu Glu His Asp

1